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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
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Listing first 45 summaries
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Pred. No. 8 the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL	2 2 2 2	RESULT 1 BD093090 LOCUS DEFINITI		45) 1	c 41	40		36 37	. U.S	نانا نانا	2 2	C 31		28	26	c 25	C 23			c 19			c 15	c 13	12	110			1 G		د د	ი 2 F		Result No.	
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5040	CAAGGAATTTCCCT	4981	Ś
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4500	AGATGTGAACTCACCATGTTAGTGACCGTTAGATACACAGAGTGGTTTTTTTT	4441	밁
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4440	TTTGACATCTACTGATGTCACCTATTTACAGGTGTGTCCTGTGACTAGGGGGTGAAGGGA	4381	망
4440	TTTGACATCTACTGATGTCACCTATTTACAGGTGTGTGTG	4381	Ş
4380	TAGATTTACTTACAGGGAAATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTCACAAC	4321	Дb
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N	TCTCCCTTCCATCCTGGCTGAAGCAACAAATAAAATATTTTTATGAAACACATTTTGAGT	4261	D
4320	TCTCCCTTCCATCCTGGCTGAAGCAACAAATAAAATATTTTTATGAAACACATTTTGAGT	4261	ş
26	CACAGATGTTAGCCGCTCTCGGGCTAAGTAAAGGAAGAGAATGTCAAGTTTTAAATAGCT	4201	D
4260	CACAGATGTTAGCCGCTCTCGGGCTAAGTAAAGGAAGAGAATGTCAAGTTTTAAATAGCT	4201	Ş
4200	TGGAGCAAGCTGTTTGATTTTGGCTGGGGCTCAGGCCCGGCCTGTTTGTGAATTTCACAATTT	4141	D
4200	TGGAGCAAGCTGTTTGATTTGGCTGGGGCTCAGGCCGGCC	4141	Ś
4140	GCAATTAACAAATCTATAATTAATTAGTTAAGCAATCTTCCCTTTAAGTTTAAGATTTTTG	4081	В
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	582	멅
1 ATTATGAATGTGTCAGCTGTGTACAAAGAACAATTCCTCCTTGTTTAGTCAGCACAGT	582	9
1 CCAGCGGTGAGTTTGAATGTGACATAACTTCTCTCAAAACTTAATTGAAGTGCCTTGTGT	•	벍
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1 GGAAATGAATTTTGAAACTTCACGGTGTGCCACCCTACAGTACTGCCCTGACCCCTTACA		₽
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1 AGGTATITGTGTATATITTATATATATTGTTCTCCGTTCGTTGATATCAAAGACAGTTGAA	564	₽
1 AGGTATTTGTGTATATTTTATATATATTGTTCTCCGTTCGTT	564	8
1 TGTCTGATAGCATTTGACCCTATTGCTTTTAGCCTCCCGGCTTTATATCTATATATA	558	2
1 TGTCTGATAGCATTTGACCCTATTGCTTTTAGCCTCCCGGCTTTATATCTATATATA	558	9
1 TCAAGAAACGCTCCGCCTCTTTGCAAATATGTATGAAGGAGAGAGTGCCTAAACTTCTA	552	닭
1 TCAAGAAACGCTCCGCCTCTTTGCAAATATGTATGAAGGAGAGAGA	552	9
1 GCTGGTAAGAATCGAGTGTTTATGAAGTTTTAGTCAATTGATGAATCTCATTGGCTAAAA	546	ā
1 GCTGGTAAGAATCGAGTGTTTATGAAGTTTTAGTCAATTGATGAATCTCATTGGCTAA	546	9
1 TACGTCAAGGACTCTGAAGCCGTGAGAAGAGGGAGGAACAACAACAGTAGAGGATGCCCC	540	9
1 TACGTCAAGGACTCTGAAGCCGTGAGAGAGGGGGGGAAGAACAACAGTAGAGGATGCC	540	9
1 GAGATCAGAAGTTCAGAGATGCCTCCCAGCTCCAAATTGCCAACAACAAGTGTGGCTACT	534	2
1 GAGATCAGAAGTTCAGAGATGCCTCCAGCTCCAAATTGCCAACAACAAGTGTGGCTAC	534	ß
1 AAAGTCCAGGCTGCTGAAATTAAACTCTGATGCCATTCATGCCAGCATCCAATCACGACA	528	<u> </u>
1 ARAGTCCAGGCTGCTGARATTARACTCTGATGCCATTCATGCCAGCATCCAATCACGA	528	ß
79	522	<u> </u>
1 TACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGACACTCATCAGCTCAGTTCAGTTA	522	g
1 ACAAAACATTTTAGCCCCAGAAATAGTCACAGAAATCCTCAAATCAAACCAGTATCCAG	516	밁
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1 CGGGGAGGGAAATAGATGAAAAAAAAAAAAAAAAAAAAA	510	맑
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1 GTCTTTGCTATTTGAGATTGTGACCACAACAGGCGGTTGGCTGAAAGGGAAACTGAAGGG	504	문

RESULT 2 AC078809/c LOCUS DEFINITION

ACCESSION VERSION KEYWORDS SOURCE AC078809 162646 bp DNA linear PRI 25-JAN-2003 Homo sapiens 3 BAC RPI1-600G3 (Roswell Park Cancer Institute Human BAC Library) complete sequence. AC078809 GI:19033390 HTG.

JEST AVAILABLE COP

AUTHORS TITLE JOURNAL REFERENCE AUTHORS	TITLE JOURNAL REFERENCE	AUTHORS TITLE JOURNAL REFERENCE	TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL REFERENCE		ORGANISM REFERENCE AUTHORS
Worley,K.C. Direct Submission Submitted (30-AUG-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 6 (bases 1 to 162646) Worley,K.C.	Mortey, K.C. Direct Submitssion , Submitted (29-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 165646)	Worley.K.C. Direct Submission Direct Submission Submitted (01-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Baylor Plaza, Houston, TX 77030, USA	Direct Submission Unpublished 2 (bases 1 to 162646) 2 (bases 1 to 162646) Worley, K.C. Direct Submission Submitted (04-AUG-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 162646)	Barbatla J., Benton J., Binage, K., Blankenburg, K., Bonnin, D., Blouck, J., Bowie, S., Brieva, M., Brown, E., Bryon, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Cren, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Havid, P., Hale, S., Hamilton, K., Harris, C., Harris, R., Havid, P., Hale, S., Hamilton, K., Harris, C., Harris, R., Hall, R., Martin, R., Martin, R., Martindale, J., Jackson, B., Kelly, S., Khan, U., King, L., Korvat, J., Johnson, R., Jolivet, S., Johnson, R., Jolivet, S., Johnson, R., David, R., Martindale, A., Martindale, R., Martindale, R., Martindale, A., Martindale, A., Martindale, A., Martindale, A., Martindale, T., Mabhabat, K., Maylor, M., Martindale, T., Martind	Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 162646) 1 (bases 1 to 162646) Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C.,

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COMMENT
                                                                                                                                                                   TITLE
JOURNAL
Direct Submission
Submitted (25-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Mar 1, 2002 this sequence version replaced gi:17977513.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-heip@bcm.tmc.edu/
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:

http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

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PEATURES
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Matches 5676; Conserv
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

B 1 (bases 1 to 5676)

B 21 (bases 1 to 5676)

S Sakai, T., Kagaya, S., Sato, T., Sukenaga, Y. and Fujii, H.
Gene encoding promoter region of tumor suppressor gene p51

L Patent: W0 0100818-A 1 04-JAN-2001;

TOSHIYUKI SAKAI, MIPPON KAYAKU KK, SHIGEHIDE KAGAYA, TAKAMICHI SATO,
YOSHIYAKI SUKENAGA, HIDEJI FUJII
OS HOMO Sapiens (human)
PN W0 0100818-A/1
PD 04-JAN-2001
PF 28-JUN-2000 W0 2000JP004261
PR 29-JUN-1999 JP 99P 183195
PI TOSHIYUKI SAKAI, SHIGEHIDE KAGAYA, TAKAMICHI SATO, YOSHIKAZU PI
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PI HIDEJI FUJII

PC C12N15/10,C12N5/10,C12Q1/68,A61K48/00,A61K45/00,A61P43/00,
A61P35/00

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Gene encoding promoter region
BD093089 GI:22638677
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Homo sapiens
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#0 0100818-A/1

04-JAN-2001

28-JUN-2000 WO 2000JP004261

29-JUN-1999 JP 99P 183195

TOSHIYUKI SAKAI, SHIGEHIDE KAGAYA, TAKAMICHI SATO, YOSHIKAZU
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FEATURES source	·	COMMENT	REFERENCE AUTHORS	SOURCE ORGANISM	TX o	Qy 564 Db 3	Qу 558 Db 9	Qy 5521 Db 156	Qy 5461 Др 216	Qy 5401 Db 276	Qy 5341 рь 336	Qy 5281 Db 396	Qy 522 Db 45	Qy 5161 ρb 516	Qy 5101 Db 576
A61P35/00 CC Location/Qualifiers. FH Key Location/Qualifiers 15676 /organism="Homo sapiens"	PD 04-JAN-2001 PF 28-JUN-2000 WC 2000JP004261 PF 29-JUN-1999 JP 99P 183195 PI TOSHIYUKI SAKAI, SHIGEHIDE KAGAYA, TAKAMICHI SATO, YOSHIKAZU PI SUKENAGA, PI HIDEJI FUJII PC C12N15/10,C12N5/10,C12Q1/68,A61K48/00,A61K45/00,A61P43/C0, PC	GAYA, TAKAMIC	Fujii, F	hordata; Craniata; Vertebrata; Bute	BD093092 S676 bp RNA linear PAT 27-AUG-2002 Gene encoding promoter region of tumor suppressor gene p51. BD093092.1 GI:22638680	1 AGGTATITGTGTATATITATATAATTGTTCTCCGT 5676 	1 TGTCTGATAGCATTTGACCCTATTGCTTTTAGCCTCCCGGCTTTATATCTATATATA	21 TCAAGANACGCTCCGCCTCTTTGCAAATATGTRTGAAGGAGAGAGAGTGCCTAAACTTCTA 5580	1 GCTGGTAAGAATCGAGTGTTFATGAAGTTTTAGTCAATTGATGAATCTCATTGGCTAAAA 5520 	1 TACGTCAAGGACTCTGAAGCCGTGAGAAGAGGGGGGAAGAACAACAGTAGAGAGGATGCCCA 5460 	1 GAGATCAGAAGTTCAGAGATGCCTCCAGCTCCAAATTGCCAACAACAACAAGTGTGGCTACTA 5400 	11 AAAGTCCAGGCTGCTGAAATTAAACTCTGATGCCATTCATGCCAGCATCCAATCACGACA 5340 	1 TACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGACACTCATCAGCTCAGTTCAGTTACA 5280 	1 ACAAAACATTTTAGCCCCAGAAATAGTCACAGAAATCCTCAAATCAAACCAGTATCCAGA 5220 	CGGGGACGGAAGGAAATAGATGAAAAAAAAAAAAAAAAA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (20-NoV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 7703, USA
On Nov 20, 2002 this sequence version replaced gi:24080629.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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3 (bases 1 to 160574)
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Rat Genome Sequencing Consortium.
Direct Submission
                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length

(see http://www.bgsc.bcm.tmc.edn/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently

consists of 4 contigs. The true order of the pieces

is not known and their order in this sequence record is

arbitrary. Gaps between the contigs are represented as

runs of N, but the exact sizes of the gaps are unknown.

This record will be updated with the finished sequence

as soon as it is available and the accession number will

be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: KBUG
Center clone name: CH230-436C20
Center clone name: CH230-436C20
Center clone name: CH230-436C20

Resembly program: Phrap; version 0.990329
Consensus quality: 151333 bases at least 030
Consensus quality: 153444 bases at least 030
Consensus quality: 154259 bases at least 020
Retimated insert size: 155447; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center code: BCM
Web Site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu
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                                            93078
93178
113866
113966
93077: contig of 93077 bp in le
93177: gap of unknown length
113865: contig of 20688 bp in le
113965: gap of unknown length
158782: contig of 44817 bp in le
158882: gap of unknown length
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ACCTATTTACAGGIGTGTGCCTGIGACTAGGGGGTGAAGGGAAGATGIGAACICACCATGI ATGTCAGATTTCT-----CTTCAGCTTGTCTCACAACTTTGACATTTTCTGATGTC ATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTCACAACTTTGACATCTACTGATGTC AGAACAACAAATAAAACATCTTTATG-AACACATTTTGAACCAGAATTTCTTACAAGAAA GAAGCAACAAATAAAATATTTTATGAAACACATTTTGAGTTAGATTTACCAGGGAA 4339 ĊAĠŢĊŢĠĀĠĠĀĀĀĠĠĀĀĠĀĀĠĀĀŢĊŢĊĀĀĠŢŢŢŢĀĀĀĀŢĀĠĊŢŢĊŢĊ-----ĊĊŢĠĠĊŢ CGGGCTAAGTAAAGGAAGAATGTCAAGTTTTAAATAGCTTCTCCCTTCCATCCTGGCT

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64926 CAGCGACATTIGGGCACACGG-----CTCTATTICCCTCTIGGACTCTATTCTAATTT

TAGTGACCGTTAGATACACAGAGTGGTTTTTTTTCCCCCCTGTTGGAGTCTATCCTAACTG ACTAGTTTGCAGGTGT---CTATGACTACGGCATGAATGG-AGATATGTACTTAGCATGT

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TTGGGAATATATGAACAAITTTATGGTTTCCTTTCGAAGTAGGTCAAAGTCAAAGCAAAAC 4698

TCTTCACTATATAAACAAATGCCAGATTTTAGAGTAGGTAAGTCAAGGGAGACTAAGAG

CCATATTCAGAAAGGAAATAAATTATTTTGTGTGTAGACTTT-CCTGATATTACACTGAT AGCTTCTGAATCATATTTCATTTCAATTTCCAAATCCACAAAACCAGGATAAGTTTACAGC

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Best Local Similarity
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                                                                       65264
                                                                                                                                                                                                             65379 GGCCATAGCTACAGGACATTAGTTATTCTCAATTTAAGAACTTTGCAATCGGGTCATCTG
                                                                                                                                           65319
   65204
                                                                                                      4100
                                                                                                                                                             4041 TATTTGCTAATAGCAGGGAAGAAGACCCAAACTCTTTAACTGCAATTAA-CAAATCTATAA 4099
                                                                                                                                                                                                                                    3981 GGCTGTGGTCACAGGAAATTGATTATTTTAATTTCAGAACCTTCTATTTAGGTCATCTA 4040
                                                                                         TTAATTAGTTAAGCAATCTTCCCCTTTAAGTTTTACATTTTGTGGAGCAAGCTGTTTGATT 4159
   TGGCTGGGGCTCAGGCCCCCATGTGTGTGAGATTTCACAATTCACAGATGTTAGACACGCT
                         TOGCTOGGGCTCAGGCCGGCCTGTTTGTGAATTTTCACAATTCACAGATGTTAGCCGCTCT 4219
                                                                       TTAATTAGTGAAATGATCTTTGCTTCAAGCTTCACATTTTTTAGAAAAAGCTCTCTGATT
                                                                                                                                         TATTTGCT----CAGAGAAGAAGTCAAACACTTCAATTCCAATGAAGCAAATCTATAA
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                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                      end sequence:BZ203758"
93178. ,96221
/note="wgs end_extension
clone_end:Sp6"
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complement(90372...912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-436C20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. .160574
                                                                                                                                                                                                                                                                                                                                                                                                                                              site:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              160574: contig of 1692 bp
                                                                                                                                                                                                                                                                                                    14.1%; Score 843.2; DB 2; 70.3%; Pred. No. 3.9e-151;
                                                                                                                                                                                                                                                                                       Mismatches 488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .91276)
                                                                                                                                                                                                                                                                                                                          DB 2;
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4699 CAAAAACAGCAAAAAACTGTAAGACATAAAGAATAGAGTGGAGCCGACTGAGAGATTAAAA 4758

CAACTAAAAGTGAGACGTAAGAGAATAAGACAGACTGATAGAGTTTGAGGTCAACTTTAT

Ś 밁 Ś 밁 ঠ 밁 ş 밁 Ś ş 밁 S B Ś 밁 S В S ð 밁 밁 덩 Ś ₽ 몽 Q Ő g S δ 음 중 밁 5676 TICGITGATATCAAAGACAGITGAAGGAAATGAAITITGAAACTTCACGGTGTGCGCACCC 5735 64165 64225 64276 5376 64105 64513 64573 TAAGAAGCATTATGAAAGAAAACATTAACGTATTAACTCCTATTTTAATATCACATTAAA 64514 4939 CGGGTCAGGCAAAGCTTCTAAGGGGATGTGAAAAGGGATATCTCTTTTCTCT------4988 4879 GTACATGIGCATGIGTITGAGGIAGGATATITAACTCAATAAAGGITATTTTCTTTTTATT 4938 4819 TACAATAATATTATTTCCAATTTTAATATCTTTAAGAAAATTACTATATTATATGTAA 4878 4759 TAAACTAGAATATTTTTATTAACAGGCAATTTGAAATAATTTGTGCACTTCAGAATATTC 4818 TCCTCAAATCAAACCAGTATCCAGATACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGA 5255 AAGGAGAAGTGCCTAAACTTCTATGTCTGATAGCATTTGACCCTATTGCTTTTAGCCT 5615 AGAACAACAGTAGAGAGGATGCCCAGCTGGTAAGAATCGAGTGTTTATGAAGTTTTTAGTC 5495 TTGCCAACAAGTGTGGCTACTATACGTCAAGGACTCTGAAGCCGTGAGAGGGGGGA 5435 CACTCATCAGCTCAGTTCAGTTACAAAAGTCCAGGCTGCTGAAATTAAACTCTGATGCCA 5315 AAACAAAACTICCCTAAGCAGCTCTACAAAACATTTTAGCCCCAGAAATAGTCACAGAAA 5195 ATACTATAACTTACATCT---GTATGGATAAAAATCACCACAGGCTATTTTTTTTTAATT 64457 GTTGGCTGAAAGGGAGGCTGAAGGGGGTTGGGGAGG------GGAAGAAGAGGGGG 64226 ACTTEMAGACGETGATTEGETGAAAGGAAAATGETEEGEETETTAGEAAATCTETGTA 6382 -----TAGCTGAGAGGAAGAGTGAGTTCTAAG S015 63883 6405

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	RBPERENCE AUTHORS	VERSION KEYWORDS SOURCE ORGANISM	RESULT 8 AC113784/c LOCUS DEFINITION ACCESSION	Οy 5:	Οy 51	Qy . 5	Oy 5
brooks, S., Amin, A., Anguiamo, D., A., Ayodeji, M., Baca, E., Baden, H., A., Ayodeji, M., Baca, E., Baden, H., A., Ayodeji, M., Baca, E., Baden, H., Barnstead, M., Cace, A., Calderon, E., Cavazos, I., Ceasex, H., Cece, A., Ded Davy-Carroll, L., De Anda, C., Ded Davy-Carroll, L., De Anda, C., Ded Davy-Carroll, L., Durbin, K., Duval, B., Flagg, M., Forbes, L., Foster, M., Ganta, A., Garner, T., Gill, R., Grady, M., Guerra, W., Hamil, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, Hernandez, M., Hamilton, M., Hongac, A., Hogues, H., Hoduson, N., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Levas, H., Levas, J., Longa, H., Levas, H., Levas, J., Wartin, R., Martin, R., Martinez, E., McNeill, T.Z., Menen, E., McNeill, T.Z., Menen, E., McNeill, T.Z., Menen, R., Martin, S., Mandasa, M., Murphy, M., Perez, A., Perez, L., Pfannkoch, C., Popovic, D., Primus, E., Pul, L., Popovic, D., Primus, E., Pul, L., Popovic, D., Primus, E., Pul, L., Popovic, D., Primus, S., R., Saster, S., Scott, G., Shatsman, S., Sisson, X., Soretle, R., Sasty, J., Unton, A., Svatek, A., Tabor, P., Unton, A., Svatek, A., Tabor, Z., Uniden, R., Sose, J., Unton, A., Svatek, A., Tabor, Z., Uniden, R., Sose, J., Tabor, P., Uni	es 1 to 284005) .Marie., Metzker, M.Lee., Abramzon, S	C113784.5 GI: TG; HTGS PHASE attus norvegic attus norvegic bukaryota; Meta ammalia; Euthe	AC113784 284005 bp DNA linear HTG 19-NOV-2002 Rattus norvegicus clone CH230-98F2, WORKING DRAFT SEQUENCE, 3 unordered pieces.	5916 IGIGGACATAITIICIGAATGICTITIITIGGITGAT 5951 	5856 CCTCCTTGTTIAGTCAGCACAGTGATAITATTITGGACTTTCTGTGGACTTTAAAGTGGTC 5915		5736 TACAGTACTGCCCTGACCCTTACATCCAGCGGTGAGTTTGAATGTGACATAACTTCTCTC 5795

Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Wilson,R., Wilke,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yoo,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., Yon Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Wang, J.,

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE

JOURNAL

Worley, K.C. Direct Submission

Direct Submission

Jnpublished

(bases 1 to 284005)

Submitted (05-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 284005)

REFERENCE AUTHORS TITLE JOURNAL

Rat Genome

Sequencing Consortium.

COMMENT

EST AVAILABLE COPY FEATURES misc_feature Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 19, 2002 this sequence version replaced gi:23195097. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gays filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome shorgun sequence only contigs will be indicated in the feature Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu Contact: hgsc-help@bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu/ Conter project name: GSGN Conter clone name: CH230-98F2 Conter clone name: CH230-98F2 Assembly program: Phrap; version 0.990329 Consensus quality: 249691 bases at least Q30 Consensus quality: 25242 bases at least Q30 Consensus quality: 252424 bases at least Q20 Estimated insert size: 252183; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation NOTE: This sequence may represent more than one clone. NOTE: This is a 'working drait' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved. NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html) Center: Baylor College of Medicine Center code: BCM .---- Genome Center /organism="Rattus norvegicus" /mol_type="genomic DNA" /db_xref="taxon:10116" /clone="CH230-98P2" 1. .1035 Location/ .284005 9564: contig of 9564 bp in length 9664: gap of unknown length 273939: contig of 264275 bp in length 274039: gap of unknown length 284005: contig of 9966 bp in length. 'Qualifiers estimation

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Matches 1417; Conserv
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                                                                                                                                                                                                                                       ATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTCACAACTTTGACATCTACTGATGTC
                                                                                                                                                                                                                                                                                  AGAACAACAAATAAAACATCTTTATG-AACACATTTTGAACCAGAATTTCTTACAAGAAA
                                                                                                                                                                                                                                                                                                         TGGCTGGGGCTCAGGCCCCATGTGTGTGTGAGATTCACAATTCACAGATGTTAGACACGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                    TOGCTOGGGCTCAOGCCOGCCTGTTTGTGAATTTCACAATTCACAGATGTTAGCCGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATTTGCT----CAGAGAAGAAGTCAAACACTTCAATTCCAATGAAGCAAATCTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCATAGCTACAGGACATTAGTTATTCTCAATTTAAGAACTTTGCAATCGGGTCATCTG
                                                                                                                  TAGTGACCGTTAGATACACAGAGTGGTTTTTTTTTTCCCCCCTGTTGGAGTCTATCCTAACTG 4519
                                                                                                                                                                             ACCTATTTACAGGTGTGTCCTGTGACTAGGGGGTGAAGGGAAGATGTGAACTCACCATGT
                                                                                                                                                                                                                                                                                                                                                                         COGGCTAAGTAAAGGAAGGAATGTCAAGTTTTAAATAGCTTCTCCCTTCCATCCTGGCT
                                                           AGCTTCTGAATCATATTTCATTCAATTTCCAAATCCACAAAACCAGGATAAGTTTACAGC 4579
                                                                                               CAGCGACATTICGGCACACGG-----CTCTATTICCCTCTTGGACTCTATTCTAATTT 71684
                                                                                                                                                                                                                       ATGTCAGATTTCT-----
                                    AGCTTCTGAATCATATTTCATTCAATTTCTAAATCCACAGAACCAGGATTGGTTTACGGC 71624
                                                                                                                                                            ACTAGTTTGCAGGTGT
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clone end:T7"
7353 - B173
/note="clone_boundary
clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           end sequence:BH306731"
274040. .275276
/note="wgs_end_extension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="wgs_contig"
complement(263454...2)
/note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   end_sequence:BH306729"
9665. .11350
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15329. .16533
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14183. .15278
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70.3%;
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Pred. No. 3.7e-151;
0; Mismatches 488;
                                                                                                                                                                                                                         -CTTCAGCTTGTCTCACAACTTTGACATTTTCTGATGTC
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72015 4159 72075 4099 72130

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REFERENCE	RESULT 9 AC126304/c LOCUS DEFINITION ACCESSION VERSION VERSION KEYWORDS SOURCE ORGANISM	Oy 58 Db 703 Oy 59 Db 703	.1 .1
NCE 1 (bases 1 to 204313) (ORS Marie, Marie, Metzker, M.Lee, Abramann, S., Adams, C., Alder, J., Barber, M., Barnstead, M., Benahmed, F., Barber, M., Cree, A., D'Souza, L., Cher, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Charber, M., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J., Charber, M., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, R., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, R., Chen, R., Chen, R., Chen, R., Chen, Y., Dinh, H., Divya, K., Cavaza, M., Chepser, M., Barber, M., Davis, C.A., Folter, M., Chen, P., Dederich, D., Denson, S., Derson, C.A., Dinkh, H., Divya, K., Eaves, K., Egan, A., Ender, C.A., Folter, M., Gabrer, P., Fan, G., Folter, M., Gabrer, M., Esves, C., Karler, M., Gabre, C.A., Folter, M., Gabrer, P., Fan, G., Folter, M., Gabrer, M., Gabrer, M., Gabrer, M., Gabrer, M., Gabrer, M., Gabrer, M., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, K., Harrigh, M., Guerra, M., Gebregorgis, E., Gelt, M., Hamilton, C., Hamilton, C., Hamilton, K., Harrigh, M., Guerra, M., Guevara, M., Hernandez, J., Hodgson, A., Hogues, M., Hallon, S. L., Hodgson, A., Hogues, M., Hallon, S. L., Hodgson, A., Hogues, M., Karpathy, S., Kelly, S., Kally, S.,	AC126304 AC126304 Rattus norvegicus clone CH230-244D17, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces. AC126304 AC12	5856 CCTCCTTGTTTAGTCAGGACAGTGATATTATTTTGGACTTTTCTGTGACTTTAAAGTGGTC 5915	TACAGTACTGCCCTGACCCTTACATCCAGCGGTGAGTTTGAATGTGACATAACTTCCTC

REFERENCE AUTHORS TITLE JOURNAL

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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projecte/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23907953. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 204313)
Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (05-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 204313)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                        as soon as it is available and the accession number will be preserved.
                                                                                                                                                                    71915
72015
203207
203307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----- Genome Center
complement (4101. .4830)
                   1. .204313
/organism="Rattus norvegicus"
/organism="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-244D17"
                                                                                                                                             ocati
                                                                                                                                                              71914: contig of 71914 bp in length
72014: gap of unknown length
203206: contig of 131192 bp in length
203306: gap of unknown length
204313: contig of 1007 bp in length.
                                                                                                                                           Qualifiers
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63776
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63891 TATTTIGCT----CAGAGAAAGAAAGTCAAACACTTCAATTCCAATGAAGCAAATCTATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63951 GCCCATAGCTACAGGACATTAGTTATTCTCAATTTAAGAACTTTGCAATCGGGTCATCTG
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Similarity 70.0%;
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                           CAACTAAAAGTGAGACGTAAGAGAATAAGACAGACTGATAGAGTTTGAGGTCAACTTTAT
                                                                           CAAAAACAGCAAAAACTGTAAGACATAAAGAATAGAGTGGAGCCGACTGAGAGATTAAAA
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72015. .73525
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Pred. No. 9.9e-150;
0; Mismatches 493;
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FEATURES

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5855	9
5795 62155	73
5735 62215	67
5675 62275	16 CCCGGCTITATATCTATATATACACAGGTATTTGTGTATATTTTATATAATTGTTCTCCG
5615 62335	556 AAGGAGAGAAGTGCCTAAACTTCTATGTCTGATAGCATTTGACCCTATTGCTTTTAGCCT
5555 62395	496 AATTGATGAATCTCATTGGCTAAAATCAAGAAAGCTCCGCCTCTTTGCAAATATGTATG
5495 62455	5436 AGAACAACAGTAGAGAGGATGCCCAGCTGGTAAGAATCGAGTGTTTATGAAGTTTTAGTC
5435 62515	376 TIGGCAACAAGAGIGTGGCTACTATACGTCAAGGACTCTGAAGCCGTGAGAGAGGGGGGA
5375 62570	316 TTCATGCCAGCATCCAATCACGACAGAGATCAGAAGTTCAGAGATGCCTCCAGCTCCAAA
5315 62625	6 CACTCATCAGCTCAGTTCAGTTACAAAAGTCCAGGCTGCTGAAATTAAACTCTGATGCCA
	196 TCCTCAAATCAAACCAGTATCCAGATACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGA
5195 62738	136 ANACAAAACTTCCCTAAGCAGCTCTACAAAACATTTTAGCCCCAGAAATAGTCACAGAAA
5135 62798	
w ~	5016 TIAAATATAATCAAGGAATTICCCTGTCTITGCTATITGAGAITGTGACCACAACAGGCG
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4988 62969	39 CGGGTCAGGCAAAGCTTCTAAGGGGATGTGAAAGGGATATCTCTTTCTCT
4938 63C29	~ ~
4878 63086	4819 TACAATAATATATTATCCAATTTTAATATCTTTAAGAAAATTACTATATTATATGTAA
4818 63146	9 TAAACTAGAATATITTTATTAACAGGCAATTTGAAATAATTTGTGCACTTCAGAATATTC

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ice 2 (bases 1 to 214853)

Birren, B., Linton, L., Nubaum, C., Lander, E., Ali, A., Allen, N., Alder, B., Linton, L., Nubaum, C., Lander, E., Ali, A., Allen, N., Alder, B., Linton, L., Nubaum, C., Lander, E., Ali, A., Allen, N., Alder, B., Erren, S., Bartan, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Cooke, P., DeArellano, K., Collins, S., Collywore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faxo, S., Ferreira, P., Fitzhyh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Cord, S., Goyette, M., Graham, L., Ohnson, R., Jonnes, C., Kamat, A., Kartas, A., Kells, C., Lakocque, K., Lanazaree, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., Nachean, C., McCarthy, M., McRean, P., McKernan, K., Holdin, J., Meneus, L., Mihova, T., McRenan, P., McKernan, K., Pelerson, K., Phunkhang, P., Peterson, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., McCarthy, M., Sarlos, R., Sabuer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Sange-Thomann, N., Schupback, R., Seamoni, R., Saloner, S., Schupback, R., Seamoni, R., Shauer, S., Schupback, R., Seamoni, N., Strauss, N., Travers, M., Travis, N., Trigillo, J., Vassillev, H., Viel, R., Vo, A., Wilson, B., Wa, X., Wyman, D., Ye, W.J., Young, G., Direct Submission

Jirect Submission

Submitted (25-FEB-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (bases) to 214653)

RS Birera, B., Nusbaum, C. and Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H. M., Barna, K., Bastien, V., Bloom, T., Bubmisted (05-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

2 (bases) to 214653)

RS Birera, Submission

Submitted (05-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

2 (bases) to 214653)

RS Birera, Submission

Submitted (05-SEP-2008) Whitehead Institute/MIT Center for Genome Research, 320 Cooke, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62154
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Mus musculus (house mouse)
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Bukaryota, Metazoa, Chordata, Sciurognathi, Muridae, Murinae, Mus.
1 (bases 1 to 214853)
Birren, B., Nusbaum, C. and Lander, E.
Mus musculus Chromosome 16, clone RP23-186N8
Unpublished
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Mus musculus chromosome
AC113020
AC113020.9 GI:37515087
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All repeate were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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complement(9899. .10500)
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52...57
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                                                                        family="(TTTTG)n"
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complement(22556..25200)
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21157. .2
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/rpt_family="L1"
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                14.C%; Score 835.4; DB 10; 70.2%; Pred. No. 1.2e-149; tive 0; Mismatches 471;
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4989	4879 GTACATGTGCATGTGTTTTGAGGIAGGATATTTAACTCAATAAAGGTTATTTTCTTTTATT 4938	4759 TAAACTAGAATATTTTATTAACAGGCAATTTGAAAATAATTGTGCACTTCAGAATATTC 4818 52546 AAACTTTATTTTTTCCCCATTGACAGGCCATCTAAAATAATTCATAAATAA		4519 GAGCTTCTGAATCATATTCATTCAATTCCAAATCCACAAAACCAGGATAAATTACAG 4578	4399 CACCTATTTACAGGTGTTCCTGTGACTAGGGGGATGAGGGAAGATGTGAACTCACCATG 4458		51984 TIGGCTIGGAGCCGGCATGTGTGTGTGAGTTTCACAATTCACAAGTGTTAGACACGC 52043 4219 TCGGGCTAAGGAAAGGAAAGTCCAAGTTTAAATAGCTTCTCCCTCC	51869 TATTTGCTCAGAGGAAGAAAGCCAAACAC-TTGATTCCAATGAGCAAATCTATAAT 51923 4101 TAATTAGTTAAGCAATCTTCCCTTTAAGTTTTACATTTTGTGGAGCAAGCTGTTTGAT 4158	3981 GGCTGTGGTCACAGGAAATTGATTATTATATTTCAGAACCTTCTATTTAGGTCATCTA 4040
RESULT 11 HSP63G01 LOCUS HSP63GC1 835 bp DNA linear PRI 04-JAN-2001 DEFINITION Homo sapiens P63 protein (P63) gene, exon 1. ACCESSION AF124528	OY 5888 TIGGACTITICITORGACTITALAGTGGTCTGTGGACATATTTTCTGAATGTCTTTTTTGGT 5947	5768 53603 5828 53663	Qy 5648 TGTGTATATTTATATATTCTTCTCGTTGTTGTATAGAAGAAGTTGAAGGAAATG 5707	OY 528 ACGCCCCCCTCTTTGCAARTATGTATGAAGGAGAAGTGCCTAAACTTCTATGTCTCA 5587	53244 AGGGCTCTAAAACTGTGGCAGA-GAGGAAGAACAGCTTTACAGGGGGTGCCCAGCTGGTA 5468 AGAATCGAGTGTTATGAAGTTTTAGTCAATTGATGATCTCATTGGCTAAAATCAAGAA [5313 TOGOTTCTGTGATTAAACTCTGATGCCATTCAAACTACAAGTGCCCAATCCCAAGCAAG	Db 53020 ĀTĪGTĀĞCCACĀĞCAGAACĪĞĀĞAGĀGĀGĀGĀGĀĀTĀČĀĀĀĀĀĀĀĀĀĀĞĀ 53079 Qy 5228 AAGTGTTATGTAGCTGGAGCAGGGTGGACACTCATCAGCTCAGTTCAGTTACAAAAGTCC 5287	5108 GGAGGAAATAGATGAAAAAAAAAAAAAAAAAAATTCCCTAAGCAGCTCTACAAAAC 	Db 52845 CTCGTTGAAATGAAGAGTGCGGTTCTAGGTTAAATATAATCAAGGAATTTCCCTGTCTTTG 52904 52845 CTCGTTGAAATGAAGAGTGCTGGTCTAAGTAAATATAATCAAGGAATTTCCCCTGTCTTTG 52904 CTATTTGAGATTGTGACCACAACAGGCGGTTGGCTGAAAAGGGAAACTGAAGGGGGGAG 5107 Db 52905 CTATTTGAGATTCTGACCACAAAGGGGTTGGCTGAAAAGGGAAGCACAAAAGGGGGGGG

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Best Local Similarity 100.0%; Pred. No. 3.7e-85;
Matches 499; Conservative 0; Mismatches 0;
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1 (bases 1 to 835)

Yang,A., Kaghad,M., Wang,Y., Gillett,E., Fleming,M.D., Dotsch,V., Andrews,N.C., Cagut,D. and McKeon,F.

p63, a bomolog at 3q27-29, encodes multiple products with transactivating, death-inducing, and dominant-negative activities mol. Cell 2 (3), 305-316 (1998)
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National Cancer Institute, Building 37, Room 2C22, 37 Convent
Drive, Betheeda, MD 20892, USA
Location/Qualifiers
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                                                                                                                                                                                                                                                          GICTGATAGCATTTGACCCTATTGCTTTTAGCCTCCCGGCTTTATATCTATATACACA
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                                                                                                                                                             CAGCGGTGAGTTTGAATGTGACATAACTTCTCTCAAAACTTAATTGAAGTGCCTTGTGTA 582:
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                                                                   ATTATTTTGGACTTTCTGTGGACTTAAAGTGGTCTGTGGACATATTTTCTGAATGTCTTT 5941
                   TTTGGTTGATATTTGGATC 5960
       TTTGGTTGATATTTGGATC
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216. .305
216. .305
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Homo sapiens P63 protein alternatively spliced. AY339663 AY339663.1 GI:34304685
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Mammalia; Eutheria; Primates;
1 (bases 1 to 531)
Vieira,A.R. and Murray,J.C.
Sequencing of Candidate Goreg
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Direct Submission
Submitted (10-JUL-2003) Pediatrics,
Iowa City, IA 52242, USA
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Similarity 99.8%;
71; Conservative (
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                                                       ATGTATGAAGGAGAGAAGTGCCTAAACTTCTATGTCTGATAGCATTTGACCCCTATTGCTT
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            GCCACCCTACAGTACTGCCCTGACCCCTTACATCCAGCGGTGAGTTTGAATGTGACATAAC
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/db_xref="G1:34304695"
/translation="MNFETSRCATLQYCPDPYIQR"
/218. .279
/number=1
/14
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
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Pred. No. 1.1e-79;
0; Mismatches 1;
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Catarrhini; Hominidae;
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	TITLE JOURNAL COMMENT	RESULT 13 ACO91240/c LOCUS DEFINITION ACCESSION VERSION ACCESSION CETANORDS SOURCE ORGANISM ORGANISM TITLE JOURNAL REFERENCE AUTHORS AUTHORS AUTHORS	2 2 2 2 2
http://ftp.genome.washington.edu/RM/RepeatMasker.html		AC091240 AC091240 Mus musculus clone RP23-16N1, LOW-PASS SEQUENCE SAMPLING. AC091240.1 GI:13560417 HTG; HTGS PHASEO. Mus musculus (house mouse) Mixaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 56268) Birren, B., Linton, L., Musbaum, C. and Lander, E. Mus musculus, Clone RP23-16N1 1 (bases 1 to 56268) Birren, B., Linton, L., Musbaum, C., Lander, B., Allen, N., Anderson, S., Bairan, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Collagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagoe, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K.,	5789 TICTCTCNAAACTTAATTGAAGTGCCTTGTGTATTATGAATGTGTCAGCTGTGTACAAAG 5848
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Query Match 6.7%;
Best Local Similarity 68.3%;
Matches 541; Conservative
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                                                                                                                                                                                                                                                                                                                             5581
 Tabaska, J.E. and Zhang, M.Q. Detection of polyadenylation signals Gene 231 (1-2), 77-86 (1999)
                                             Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Butheria; Rodentia;
                                                                                                       AF533892 208158 bp DNA linear ROD 31-JUL-2003
Mus musculus p63 (Trp63) gene, alternatively spliced, complete cds.
AF533892
AF533892.1 GI:32812140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAGATCAGAAGTTCAGAGATGCCTCCAGCTCCAAATTGCCAACAACAGTGTGGGCTACTA 5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCAAAACATTGTAGCCACAGCAGAACTGACAGGAGCTCTCAAAATCAAGTCAGAATACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACAAAACATTTTAGCCCCAGAAATAGTCACAGAAATCCTCAAATCAAACCAGTATCCAGA 5220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGGGGAGGGAAATAGATGAAAAAACAAAACAAAACATTCCCTAAGCAGCTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCTTTGCTATTTGAGATTGTGACCACAACAGGCGGTTGGCTGAAAGGGGGCAGAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGITATTTTCTTTTATTCGGGTCAGGCAAAGCTTCTAAGGGGGATGTGAAAGGGATATCT
                                                                                                                                                                                                                                                                                                                                                                                                  GCTGGTAAGAATCGAGTGTTTATGAAGTTTTAGTCAATTGATGAATCTCATTGGCTAAAA 5520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARAGICCAGGCIGCIGARAITAAACTCIGAIGCCAITCAIGCCAGCAICCAAICACGACA 5340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GĠŢĠĠĠĠŢĠĠĠĠ-----CĂĠĠĠĂĠĂĀĠĊĊĠĀĠŖĀĀĀĀĀĀĀĀĀĀĀĞĊĠŢĊŢĊŢ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTCTTTGCTATTTGAGATTGTGACCACACAGGCGGTTGGCTGAAAGGGAAACTGAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGACACTCATCAGCTCAGTTCAGTTACA 5280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTTCTCTTAGCTGAGAGGGAAGAGTGAGTTCTAAGTTAAATATAATCAAGGAATTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAATGAATTT 5712
                                                                                                                                                                                                                                                     TCAAGAAACGCTCCGCCTCTTTGCAAATATGTATGAAGGAGAGAAGTGCCTAAACTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TACGTCAAGGGCTCTAAAAACTGTGGCAGA-GAGGAAGAACAGCTTTACAGGGGGTGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGAAATGAATTT 26597
                                                                                                                                                                                                                                                                                                                                                      GGAAGAAACGCCCCGCCTCTTTGCAAATCTGAGTAAAGGGGGGAAGTGTCTAAACTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGATCAGAAGTTCAGAGATGCCTACAAATTGC-----CAACAAGTGTGGCCACTC
                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
              ij
              human DNA
              sequences
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26789

9888

5640

26729

26669

5700

26609

26849

26908

26959

27019

27072

5160

27187 5100

27132

27247 5040 4980

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REFERENCE
AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ETU'S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 208158)
2 (bases 1) to 208158)
5 (st.) Wang, J.H., Zhang, M.Q. and Mills, A.A.
Direct Submission
Submitted (02-AUG-2002) Mills Lab, Cold Spring Harbor Laboratory, 1
Bungtown Rd, Cold Spring Harbor, NY 11724, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99250252
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178277. .178463,179678. .179793,181332. .181441,
182160. .182296,184252. .18434,187033. .187219,
198613. .198770,200897. .201041,205091. .205106)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   //note="yrionym: P63"
join(<1: .209,79122: .79250,80020: .80152,136373
join(<1: .19863,179678: .179793,181332: .181441,
178277: .178463,179678: .179793,181332: .187219,
182160: .182296,184252: .184334,187083: .187219,
198613: .198770,200897: .201041,202292: .202385,
205091: .208158)</pre>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              joncte-"alternatively spliced"

join(<1 . .209,79122 . .79250,80020 . .80152,136373.

178277 . .178463,179678 . .179793,181332 . .181441,

182160 . .182284,184252 . .184334,187083 . .187219,
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/product="alternatively spliced"

join(<1. 209,79122. .79250,80020. .80152,136373.

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198613. .198770,200897. .201041,205091. .>208158)
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mol type="genomic DNA"

db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="Trp63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="p63 TA gamma"
note="alternatively spliced"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="transactivating isoform; partially characterized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="Trp63"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="transactivating isoform only"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          product="p63 TA beta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome= "16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5' RACE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .80152,136373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .136627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .136627,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .136627
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                 SG
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                                                                                                                                                                                   5'UIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                       , note="first exon in DN isotypes;
transactivating isoform"
/number-3,
                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="alternatively spliced"
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using 5' RACE"
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                                                                                                                                                                                                                                                                                                                                   117914. .118099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               jobn(117914. .118099,136373. .136627,178277. .178
179678. .179793,181332. .181441,182160. .182296,
184252. .184334,187083. .187219,198613. .198770,
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partially characterized

spliced out of

.178463,

.178463,

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note="transactivating isoform only"
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PRI 15-OCT-2002 sequence.

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                                                                                                                                                                                                                                                                                                                                          CAGTACTGCCCTGACCCTTACATCCAGCGGTGAGTTTGAATGTGACATAACTTCTCTCAA
                                                                                                                                                                                                                                                                                                                                                                                               TGTTGGTATCAAAGAGAGTTGAAGGAAATGAATTTTGAAACTTCACGGTGTGCCACCCTA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CGCCTTTATATCTATATATACACAGGIATTTGTGIAIATATTTATATAATTGTTCTCCCGTT
TAGATATOTTTTCTACAGTTATCTTATACTTTATTTCTTGA
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                                                                                                                                                                                                                                                                                             CAGTACTGCCCCGACCCTTACATCCAGCGGTGAGTTTAAATCTGACCTGGCGTCTGTCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGCTACATACCTAGATATTCTCAGGTGTATATGTATATTTTATAGAATTGCTTCCCATC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pred. No. 2.7e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
2.7e-42;
71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 208158;
                                               5958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2; Gaps
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                                                                                                                                                    5917
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AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
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AUTHORS
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Wang, C. and Bielicki, L.
The sequence of Homo sapiens
Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Submitted (30-MAR-2002) Genome
University School of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Submitted (29-NOV-2001) Genome
University School of Medicine,
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Sulfton, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
Submitted (15-OCT-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Sep 18, 2002 this sequence version replaced gi:19703341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (18-SEP-2002) Genome Sequencing Center, Washington
Submitted (18-SEP-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 (bases 1 to 159249)
Waterston, R.H.
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                                                                                                                                                                                           NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University, 4444 Forest 7 (bases 1 to 159249)
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Submitted (03-OCT-2002)
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                                                                                                                                                                                                                                                                                                                                             Center: Washington University Genome Sequencing Center code: WUGSC
Web site: http://genome.wustl.cdu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
Center project name: H_NH0733G06
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4444 Forest Park Parkway, St. Louis,
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Query Match Rest Local Similarity

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This sequence is not the entire insert of the clone. This clone is overlapped by AC131754 and AC096656.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MARPING INFORMATION: Mapping information for this clone was provided by Dr. John D. Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MCPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wistl.edu/gsc
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in does not meet required finishing standards. 
Location/Qualifiers
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4776. .498
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3482. .37
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5747 .5777
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5024. .5176
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4994. 5000
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6450. .6474
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1917. 2017
           /rpt_family="(TG)n"
6998. 7244
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2218. .2499
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/db_xref="taxon:9606"
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                                                                                                                     85766 TGSTGGCTTCTGCCTGAACTCCCAGCACTTTGGGAGGCCAAGGTGGGAGGATCCTTTGAG 85707
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3413 CAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGGAAGCT 3472
                                                                            /rpt_family="Alu"
17670. .)7867
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7948. .8299
/rpt_family="MER2_type"
8868. .9128
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22342. .22558
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14829. .14876
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10529. .10659
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9717. .10011
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9299. .9510
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14996. .15187
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.9. .23264
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FEATURES

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Title: Perfect score:

US-10-030-294-2 5960

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Scoring table: Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext

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Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Total number of hits satisfying chosen parameters:

682709 seqs, 277475446 residues

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September 27, 2004, 07:46:34 ; Search time 363 Seconds (without alignments) 9111.590 Million cell updates/sec
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2: /cgn2_6/ptcdata/2/ina/5B_COMB.seq;*

3: /cgn2_6/ptcdata/2/ina/6A_COMB.seq;*

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5: /cgn2_6/ptcdata/2/ina/backfIles1.seq;*

6: /cgn2_6/ptcdata/2/ina/backfIles1.seq;*
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SEQ ID NO 10
LENGTH: 8133
TYPE: DNA
ORGANISM: Homo sapiens
US-09-659-791A-10
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Sequence 10, Application US/09659791A

Patent No. 6383908

GENERAL INFORMATION:

APPLICANT: Brett P. Monia
APPLICANT: SUBAN M. Freier
ITILE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
FILE REFERENCE: RTS-0156

CURRENT HILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 90
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Best Local Similarity 74.6%;
Matches 249; Conservative
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                                                                                                                                                                                                                                                                                                                      CACCTGTAGTCCAAGCTACACAGGAAGCTGAGGCAGAAGGATCACTTGAGCCCCAGGAGGT
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                                                                                                                                      GCTGTCTCAAAAATAATAAATAAATAAATAAAATAAAC
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                                                                                                                                                                                                                                  TGAGGCTGCAGTGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAA
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                                                                                                               CCTGTCTCTAAATTAAAAAAATAAATAAATAAC
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US-09-659-791A-11
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US-09-979-906-3
US-09-521-976-9800
US-09-521-976-9800
US-09-5814-095-7
US-09-5814-095-7
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US-09-681-638-651
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US-09-881-638-651
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US-09-881-638-651
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Query Match Length DB

Pred. No.

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US-09-964-469-3
US-09-904-469-3
US-09-901-665-3
US-09-910-111-10
US-09-911-511-485
US-09-816-512-3
US-09-816-512-3
US-09-816-512-3
US-09-816-113-13-3
US-09-816-113-13-3
US-09-816-113-13-3
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RESULT 2 US-09-738-894A-3 ; Sequence 3, App

Application US/09738894A

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Length 36651;

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J Sequence 3, Application US/09964469

J Batent NO. 6579709

J GENERAL IMPORMATION:

APPLICANT: GUEGLER, KAR1 et al

TITLE OF INVENTION: ISOLARIED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROT

TITLE OF INVENTION: THERBOF

FILE REFERENCE: CL000636DIV

CURRENT APPLICATION NUMBER: US/09/964,469

CURRENT FILING DATE: 2001-09-28

FRIOR APPLICATION NUMBER: 60/208,331

PRIOR APPLICATION NUMBER: 60/208,331

PRIOR APPLICATION NUMBER: 60/208

J PRIOR FILING DATE: 2000-06-01

PRIOR APPLICATION NUMBER: 60/738,894

PRIOR FILING DATE: 2000-12-18

SOFTWARE: FASESEQ for Mindows Version 4.0

J SEQ ID NO 3

LENGTH: 36651
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GENERAL INFORMATION:
APPLICANT: GUEGLER, KAR1 et al
APPLICANT: GUEGLER, KAR1 et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THREEOF
TILE REFERENCE: CL000636
CURRENT PILLING DATE: 2000-12-18
CURRENT FILING DATE: 2000-12-18
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO. 3
SEQ ID NO. 3
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Best Local Similarity 76.6%;
Matches 249; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-964-469-3
                                                                          TYPE: DNA
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ORGANISM: Human
             ORGANISM: Human FEATURE:
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Pred. No. 1.1e-31;
O; Mismatches 73;
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KINASE PROTEINS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 36651;
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APPLICANT: DATTA, SURJIT K.
APPLICANT: DATTA, SURJIT K.
APPLICANT: DATTA, SURJIT K.
APPLICANT: DATTA, SURJIT R.
ITILE OF INVENTION: ADENOSINE DEAMINASE DEFICIENT TRANSGENIC MICHEL OF INVENTION: METHODS FOR THE USE THEREOF
FILE REFERENCE: UTSH:243
CURRENT APPLICATION NUMBER: 05/09/301,665
CURRENT PILING DATE: 1999-04-28
EARLIER APPLICATION NUMBER: 60/083,408
EARLIER FILING DATE: 1998-04-29
EARLIER APPLICATION NUMBER: 60/083,370
EARLIER APPLICATION NUMBER: 60/083,370
EARLIER APPLICATION NUMBER: 05/083,370
EARLIER FILING DATE: 1998-04-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PATENTIN DATE: 1998-04-28
ASOFTWARE: PATENTIN TONS: 4
SOFTWARE: PATENT: PATENTIN TONS: 4
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Patent No. 6207876
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                       Query Match 3.0%;
Best Local Similarity 71.8%;
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Best Local Similarity
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LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11585 GAGGCCAGAAGTTTGAGACCAGTCTAGGCAACATAGCAAGACTTTGTCTCTTAAAAA--A 1:642
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                                                                                                                                                                                                                                                                                                                                            244; Conservative
                                                                                                                                ACACTITIGGGAAGCCGGGTCGGGAGGATAGCTTTGAGTCCAGCAGTTTTGAGACCAGTCAGG 3376
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GCACTTTGTGAGGCTGAGGGAGGATCATTTGAGTCCAGGAGTTTGAGACTAGCCTGG
                                                                                                                                                                                                                  TTACCCTTCTAAGAAATAGGTGTGAGTGGCCCAGGAGGTTGGCTCACGCCTGTAATCCCA
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Pred. No. 1.1e-31;
0; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                     Score 176; DB 3; I
Pred. No. 2.9e-30;
0; Mismatches 95;
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RESULT 6
US-09-791-211-10/c
; Sequence 10, Application US/09791211
; Sequence 10, Application US/09791211
; Patent No. 6448080
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Wart
; TITLE OF INVENTION: ANTISENSE MODULATION OF WRN
; FILE REFERENCE: RTS-0205
; FILE REFERENCE: RTS-0205
; CURRENT APPLICATION NUMBER: US/09/791,211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-798-096-10/c

Sequence 10, Application US/09798096

Patent No. 639378

GENERAL INFORMATION:
APPLICANT: Donna T. Ward

APPLICANT: Andrew T. Ward

TITLE OF INVENTION: ANTISENSE MODULATION OF RECOL2 EXITITLE OF INVENTION NUMBER: US/09/798,096

CURRENT APPLICATION NUMBER: US/09/798,096

CURRENT APPLICATION NUMBER: 0501-03-01

NUMBER OF SEQ ID NOS: 89

SEQ ID NO 10

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 2.9%;
Best Local Similarity 73.2%;
Matches 254; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IENGTH: 99500
TYPE: DNA
ORGANISM: Homo sapiens
EBATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCAGGAGCCTGTCTCAAAAATAATAAATAAATAAAAAATAA 3595
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCTAAAAAAACAAAACAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCC 3455
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                                                                                                                                                                                                                                                                                                                                                                           CACCTTCTCGGGAGGCTGAGGCAGAAGGATCATCTGAGCCCAGGAGTTAGAGGCTGCAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCTACAAAAAATAAA-----AAAGITAGCCAAGCATGGTGGTACACTCCTGTAGTCT 7900
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                                                                                                                                                                                                                        ATAATAAAATACAATTAAGTTAAATAATAAAAAAATTAAAAAA 7733
                                                                                                                                                                                                                                                         GAGCAACGATCATTCTACTGCACTCCAGCCTGGATAGCTGAGCAAGACCCTGTCTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 175.4; DB 4; Pred. No. 5.9e-30; O; Mismatches B6;
                                           WRN EXPRESSION
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    ; Sequence 405, Application US/09671317
; Patent No. 6528360
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, 11ya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen, Annick
; TITLE OF INVENTION: BIALLELIC MARKERS
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US-09-671-317-485
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NUMBER OF SEQ ID NOS:
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 2.9%;
Best Local Similarity 73.2%;
Matches 251; Conservative
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LOCATION: 65469
OTHER INFORMATION: unknown
NAME/KEY: unsure
LOCATION: 65470
OTHER INFORMATION: unknown
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 87130
OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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OTHER INFORMATION: unknown
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LOCATION: 65471
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LOCATION: 65468
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                                                                                                                                                                                                                          AAAAACAAAAAAAAAAATAAATTTTAAAAATCCAAAAAATAT 44206
                                                                                                                                                                                                                                               ATAATAAATAAATAAAATAACTTTTAAAAAACAAAAATTAAT 3617
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        BIALLELIC MARKERS
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Pred. No. 3.2e-29;
0; Mismatches 83
        RELATED TO
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        GENES
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          INVOLVED
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          DRUG METABOLISM
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FILE REFERENCE: 62.US3.CIP
CURRENT APPLICATION NUMBER: US/09/671,317
CURRENT FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR APPLICATION NUMBER: US 09/536,178
PRIOR FILING DATE: 2000-03-23
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 199-03-24
PRIOR FILING DATE: 199-03-25
PRIOR FILING DATE: US 60/126,269
PRIOR FILING DATE: 199-03-25
PRIOR FILING DATE: 199-04-30
NUMBER: OF SEQ ID NOS: 977
SOFTWARE: Patent.pm
SEQ ID NO 485
LENGTH: 49312
TENGRISM: Homo sapiens
PRIOR FILING: Fortice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 45788...45965
OTHER INFORMATION: exon 5
NAME/KEY misc feature
LOCATION: 45966..49312
OTHER INFORMATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 7564
OTHER INFORMATION: 10-286-289 : polymorphic base G or C
OTHER INFORMATION: 10-286-345 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 7619
OTHER INFORMATION: 10-286-345 : polymorphic base A or T
NAME/KEY: allele
LOCATION: 7649
OTHER INFORMATION: 10-286-375 : polymorphic base A or G
NAME/KEY: allele
LOCATION: 17258
LOCATION: 17258
LOCATION: 17258
LOCATION: 17268
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LCCATION: 5466..7466
OTHER INFORMATION: 5'regulatory region
NAME/KEY: exon
LCCATION: 7467..7725
OTHER INFORMATION: exon 1
NAME/KEY: exon
LCCATION: 20256..20355
OTHER INFORMATION: exon 2
NAME/KEY: exon
                                                                      LOCATION: 45214
OTHER INFORMATION: 10-289-201 : 1
NAME/KEY: allele
LOCATION: 45741
OTHER INFORMATION: 10-290-37 : po
NAME/KEY: allele
LOCATION: 46029
OTHER INFORMATION: 10-290-326 : 1
NAME/KEY: allele
LOCATION: 46032
NAME/KEY: allele
LOCATION: 46032
                                                                                                                                                                                                                                                                 NAME/KEY: allele
LOCATION: 21590
OTHER INFORMATION: 12-421-135 :
NAME/KEY: allele
LOCATION: 21595
OTHER INFORMATION: 12-421-140 :
NAME/KEY: allele
LOCATION: 36971
OTHER INFORMATION: 10-523-232 :
LOCATION: 45214
LOCATION: 45214
LOCATION: 46032
OTHER INFORMATION: 10-290-328 : deletion of G
NAME/KEY: primer_bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: exon
LOCATION: 36905..36975
OTHER INFORMATION: exon 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IAME/KEY: exon
OCATION: 45167..45248
OTHER INFORMATION: exon 4
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    polymorphic base C

                                                                                                                                                                                                                                                                                                                                                                                      : polymorphic base A or G
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                                                                                                                                                                         polymorphic base C or
                                                                                                     polymorphic base A or G
                                                                                                                                                                                                                                            polymorphic base C
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LOCATION: 45195..45213

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OKMATI	. - .
: 3697236990	
KEY: primer bind	•. •
0	. .
EY: primer_bind	••
OTHER INFORMATION: 12-421-140.mis complement	
BY: primer_bind	
R INFORMATION: 1	•••
NAME/KEY: primer_bind	. . ,
ORMATION: 12	•••
LOCATION: 1725917277	••
R INFORMATION:	
ION: 17239. 17257	••
KEY: primer bind	•• •
76507668	. . .
EY: primer_bind	••
OTHER INFORMATION: 10-286-375.mis	
EY: primer_bi	• ••
NFORMATION:	٠.
TION: 76207	•••
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76007618	• ••
primer_bind	••
ORMATION:	•••
IOCATION: 75657583	
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ION: 75457563	
primer bind	
1610446123 ORMATION: 10-290	
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ORMATION: 10	
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4541345432	4.
primer bind	•••
9502045037	. . .
primer bind	
ORMATION: 10	
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ORMATION: 10	٠.
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ION: 21886. 21906	~. ·
NAME/KEY: primer bind	
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/KEY: primer bind	~···
ORMATION: 12	
NAME/KEY: primer_bind	
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N: 7676769	 .
NAME/KEY: primer bind	
N: 72767294	.

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LOCATION: 45202.45226
COTHER INFORMATION: 10-289-201.pxobe
NAME/KEY: misc_binding
LOCATION: 45729.45753
COTHER INFORMATION: 10-290-37.probe
NAME/KEY: misc_binding
LOCATION: 46017.46041
COTHER INFORMATION: 10-290-326.probe
US-09-671-317-485
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LOCATION: 7607.7631
COTHER INFORMATION: 10-286-345.probe
NAME/KEY: misc binding
LOCATION: 7637.7661
COTHER INFORMATION: 10-286-375.probe
NAME/KEY: misc binding
LOCATION: 17246..17270
COTHER INFORMATION: 12-425-57.probe
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Best Local
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LOCATION: 45742...45760
OTHER INFORMATION: 10-290-37.mis
NAME/KEY: primer bind
LOCATION: 46010...46028
OTHER INFORMATION: 10-290-326.mis
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LOCATION: 7552..7576
OTHER INFORMATION: 10-286-289.probe
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NAME/KEY: primer_bind
LOCATION: 46030..46048
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NAME/KEY: primer_bind
LOCATION: 45215. 45233
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OTHER INFORMATION: 12-421-140.probe NAME/KEY: misc binding LOCATION: 36959..36983
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                                                   CAAAAATAATAAATAAATAAATAACTTTTAAAAAAACCAAAAATTAATTTAAAA 3629
                                                                                                                                                                                                 TGCAGTGATCCATGAACGCGCTGCTACACTCAGTCTGGGTGACAGTGCAAGAAGCTGTCT
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CAAGAAAAAAAAAAATCATGCGGCCAAGTAAAATAATAAATTTAATTTAATCTAGCAT 43732
                                                                                                                                                                                                                                                                                                        TGGTCCCAGCTACTTAGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGGAGGTTAAAGC
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Pred. No. 3.7e-29;
0; Mismatches 136;
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; Sequence 3, Application US/09818512
; Patent No. 6537780
; GENERAL INFORMATION:
APPLICANT: BEASLEY, Ellen et al.
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN ENZYME PROTEINS, NUCLEIC TITLE OF INVENTION: HEREOF FILE REFERENCE: CLOOL192
FILE REFERENCE: CLOOL192
CURRENT APPLICATION NUMBER: US/09/818,512
CURRENT FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
$ SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-818-512-3/c
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Best Local Simi
Matches 291;
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ORGANISM: Human
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89666 AGAAAAAAAACACCAAAAACACAACAAA 89638
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Similarity 64.8%;
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                            TAAATTITAAAAACACAACACACTAGAGA 3646
                                                                                      AAGAAGCTGTCTCAAAAATAATAAATAAATAAATTAACTTTTAAAAAACAAAATTAAT
                                                                                                                                                               TGAGGCTGCAGTGATCCATGAACGCGCTGCTACACTC-----AGTCTGGGTGACAGTGC
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                                                                                                                               AGAGGTTGCAGTGAGCTGAGATCGCACCAATGCACTCCAGCCTGGTCTGGGTAACAGAGC
                                                                 Conservative
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RESULT 9
US-09-820-002-3/c
; Sequence 3, Application US/09820002
; Patent No. 6482630
; GENERAL INFORMATION:
; APPLICANT: Gan, Weiniu
; APPLICANT: Ye, Jane

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APPLICANT: Bougueleret, Lydie
APPLICANT: Bebets-Reed, Dana
APPLICANT: Selter-Cid, Luisa
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
FILE REFERENCE: 89.US2.CIP
CURRENT PILING DATE: 2000-12-28
PRIOR APPLICATION NUMBER: US 09/599.362
PRIOR PILING DATE: 2000-06-21
PRIOR PILING DATE: 1999-12-20
PRIOR FILING DATE: 1999-12-20
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NAME/KEY: misc_feature

LOCATION: (1)...(21784)

OTHER INFORMATION: n = A,T,C
US-09-820-002-3
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US-09-750-580-1/c
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APPLICANT:
APPLICANT:
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APPLICANT: Beasley, Ellen
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PROTEASE PROTEINS, AND
TITLE OF INVENTION: USBS THERBOF
FILE REFERENCE: CLOO1194
CURRENT APPLICATION NUMBER: US/09/820,002
CURRENT APPLICATION NUMBER: US/09/820,002
CURRENT FILING DATE: 2001-03-29
NUMBER OF SEG ID NOS: 16
SOCTWARE: FastSEQ for Mindows Version 4.0
SEQ ID NO
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Best Local Similarity 71.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
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5. 6455280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAGCAAGACCCCATATCTAAAAAAAAACAAAAACAAAACTTACCTGGGTATGGTTGTG 3441
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Bour, Barbara
Bihain, Bernard
Dumas Milne Edwards,
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                                                                                                                                                                                                                                                                                             Jean-Baptiste
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NAME/KEY: primer bind
LOCATION: 12029..12050
OTHER INFORMATION: 17-42.pu
NAME/KEY: primer bind
LOCATION: 12561..12603
OTHER INFORMATION: 17-42.rp complement
NAME/KEY: primer bind
LOCATION: 14992..15012
OTHER INFORMATION: 17-41.pu
NAME/KEY: primer bind
LOCATION: 15460..15482
OTHER INFORMATION: 17-41.rp complement
NAME/KEY: primer bind
LOCATION: 15407..14.rp complement
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-641.pu
NAME/KEY: primer bind
LOCATION: 42070..42090
OTHER INFORMATION: 20-641.pu
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LOCATION: 14271...15968
OTHER INFORMATION: exon 4
NAME/KEY: misc feature
LOCATION: 15965...17969
OTHER TORNATION: 3'regulatory region
NAME/KEY: allele
LOCATION: 1239
OTHER INFORMATION: 20-828-311 : polymory
NAME/KEY: allele
LOCATION: 12247
OTHER TORNATION: 17-42-319 : polymory
NAME/KEY: allele
LOCATION: 15241
LOCATION: 15241
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SEQ ID NO 1
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LOCATION: 42218
OTHER INFORMATION: 20-841-149:
NAME/KEY: allele
LOCATION: 45442
OTHER INFORMATION: 20-842-115:
NAME/KEY: allele
LOCATION: 77058
OTHER INFORMATION: 20-853-415:
NAME/KEY: primer bind
LOCATION: 929.949
OTHER INFORMATION: 20-828.pu
NAME/KEY: primer bind
LOCATION: 1357.1377
OTHER INFORMATION: 20-828.rp co
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PRIOR FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: US 60/113,686
PRIOR FILING DATE: 1998-12-22
PRIOR PPLICATION NUMBER: US 60/141,032
PRIOR FILING DATE: 1999-06-25
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LOCATION: 13641..13752
OTHER INFORMATION: exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: exon
LOCATION: 13470..13526
OTHER INFORMATION: exon
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ORGANISM: Homo sapiens
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NAMB/KEY: misc_feature
LOCATION: 10946..12946
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INFORMATION: 20-841.rp
complement
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    polymorphic base A or G

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                                                  Query Match
Best Local Similarity
                                Matches 270;
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LOCATION: 77166..77185
OOPHER INFORMATION: 20-853.rp
NAME/KEY: primer bind
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LOCATION: 76644..76664
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LOCATION: 45430..45454
OTHER INFORMATION: 20-842-115.probe
                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1227..1251
OTHER INFORMATION: 20-828-311.probe
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NAME/KEY: primer_bind
LOCATION: 77059.77077
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LOCATION: 12348..12366
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LOCATION: 12328..1234
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LOCATION: 45863..45883
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LOCATION: 12335...12359
OTHER INFORMATION: 17-42-319.probe
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OTHER INFORMATION: 20-842-115.mis complement
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THER INFORMATION: 2
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THER INFORMATION:
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COCATION: 45443..4546
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15242..15260
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AMATTTTTTAMAMAMATAGATGAGTGTGGTGGCTCATGCCTGTAMTCCCAMCACTTTGGG
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                                Score 169.8; DB 4;
Pred. No. 1e-28;
0; Mismatches 122;
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US-09-780-049-18/c
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Patent No. 6465250
GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 40000
                                                                                                                                                                                                                                                                                                                                      Matches 249;
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TITLE OF INVENTION: ANTISENSE MODULATION OF
TITLE OF INVENTION: EXPRESSION
FILE REPRENCE: RTS-0114
CURRENT APPLICATION NUMBER: US/09/780,049
CURRENT FILING DATE: 2001-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo
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                                                                                        12105
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                                                                                                                                                    CCAAAGTGGTGAAACCCCATCTCTACCAAAA-AAAAAATACAAAAATATTCTGGGCATGG
                                                                                      TRECCCTCCCCTGTGGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGAATCGCTTGAACCC
                                                                                                                aggaggttgaggtgagtgatgatccatgaacgcgctgctacact-cagtctgggtgacagt
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71.8%;
                              TTGCAGTGAGCCAAGATCATGCCACTGCACTCCAGCCTGGGTGACAGA 11986
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Pred. No. 9.7e-29;
0; Mismatches 96
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RESULT 12
US-09-780-172-18/c
US-09-780-172-18/c
Sequence 18, Application US/09780172
Patent No. 6607916
GENERAL INFORMATION:
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US-09-754-250-3
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US-09-780-172-18
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APPLICANT: Susan M. Freier
APPLICANT: Susan M. Freier
APPLICANT: Jacqueine Wyatt
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-ALPHA EXPRESSION
FILE REFERENCE: RTS-0159
CURRENT APPLICATION HUMBER: US/09/780,172
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 96
SEQ ID NO 18
LENGTH: 63000
                                                                         CURRENT APPLICATION NUMBER: US/09/754,250
CURRENT FILING DATE: 2001-01-C5
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 111282
                                                                                                                                                                                 GENERAL IMPORMATION:

APPLICANT: WEL, Ming-Hui et al

TITLE OF INVENTION: ISOLATED HUMAN PHOSPHODIESTERASE

TITLE OF INVENTION: PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN

TITLE OF INVENTION: PROSPHODIESTERASE PROTEINS, AND USES THEREOF

FILE REFERENCE: CLOOIG63
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Best Local Similarity 70.4
Matches 240; Conservative
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ORGANISM: Homo sapiens
                 ORGANISM: Human
FEATURE:
                                                             TYPE: DNA
 NAME/KEY: misc_feature
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Pred. No. 1.4e-28;
0; Mismatches 100; Indels 1
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Patent No. 6410712
GENERAL INFORMATION:
APPLICANT: Berglind Ran Olafsdottir
APPLICANT: Jeffrey Gulcher
ITILE OF INVENTION: HUMAN NARCOLEPSY GENE
FILE REFERENCE: 2345.2601-000
CURRENT EPPLICATION NUMBER: US/09/426,290
CURRENT FILING DATE: 1999-10-25
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 168575
TYPE: DNA
ORGANITSM: USM Condition
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; OTHER INFORMATION: n = A,T,C or US-09-754-250-3
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US-09-426-290-1
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Best Local Similarity 69.7%;
Matches 260; Conservative
Query Match
Best Local Similarity
                                                                                                                                                           NAME/KEY:
LOCATION:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDS
(127009)...(127130)
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(21181)...(21403)
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2.8%;
74.2%;
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 Score 169; DB 4;
Pred. No. 2.1e-28;
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Pred. No. 1.8e-28;
O; Mismatches 105;
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                 Length 168575;
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GGGTGACAGTGCAAGAAGCTGTCTCAAAATAATAA 3581 	3523 GAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAAGCTGTCTCAAAAATAATAA 	음 성
ACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCAT 3522 GCTTGAACCCAGAAGGTGGAGGTTGCAGTGAGCCAA 14046	3463 ACAGGAAGCTGAGGCAGAAGGATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCAT	§ 8
CTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTAC 3462	3403 AAAAACAAAACAAAACTAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTAC	B 8
ACCAGTCAGGGCAACACAGGAAGACCCCATATCTAA 3402 	3343 ATAGCTTGAGTCCAGCAGTTTGAGACCAGTCAGGGAACACAGCAAGAAGCCCATATCTAA	₽ Q
IGTAATCCCAACACTTIGGGAAGCCGGGTCGGGAGG 3342	3283 TAGATGAGTGGTGGCTCATGCCTGTAATCCCAACACTTTGGGAAGCCGGGTCGGGAGG	ğ Q
168.6; DB 4; Length 55827; . No. 1.7e-28; ismatches 109; Indels 7; Gaps 2;	.6; DB 4; 1.7e-28; ches 109;	Que Bes Mat
ROTEASE PROTEINS, DLECULES ENCODING HUMAN PROTEASE PROTEINS, AND 13,133A	15 813-133A-3 813-133A-3 ence 3, Application US/09813133A nt No. 6455294 RAL INFORMATION: LICANT: GAN, Weiniu et al LICANT: GAN, WEINIU ET ACTD MOLECULES ENCODING LE OF INVENTION: NUCLERIC ACTD MOLECULES ENCODING LE REFERENCE: CLOOL173 ERENT FILLING DATE: 2001-06-06 BER OF SEQ ID NOS: 4 TWARE: FastSEQ for Windows Version 4.0 ID NO 3 ID NO 3 ID NO 3 ID NO 3 ID NOS: 4 GANTSM: Human GANTSM: Human GANTSM: Human GANTSM: Human	RESULT US-09- I Sequ I Sequ GENE GENE III III III III III III III III III
. 34046 .	3588 AAAAATAACTTTTAAAAAACAAAAA 3612 	B 8
AGTGCAAGAAGCTGTCTCAAAAATAATAAATAAAT 3587 	3528 CGCTGCTACACTCAGTCTGGGTGACAGTGCAGAAGCTGTCTCAAAAATAAAT	유 &
GCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACG 3527	3468 ARGCTGAGGCAGAAGGATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACG	8 8
ATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGG 3467	3408 CAAAACAAAACAAAATTACCTGGGTATGGTTGTTGGTCGACGTGTAGTCCAAGCTACACAGG	B 8
GGGCAACACAGCAAGCCCCATATCTAAAAAAA 3407 	3350 GAGTCCAGCAGTTTGAGACCAGTCAGGCAACACAGCAAGACCCCATATCTAAAAAAA	당 &
CAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTT 3349	3290 GTGTGGTGGCTCATGCCTGTAATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTT	A 성
smatches 80; Indels 4; Gaps 2;		Mato

Search completed: September 27, 2004, 14:38:36 Job time : 367 secs

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Title:
Perfect score:
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Maximum Match 100%
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1: /cgn2 6/ptodata/2/pubpna/USO7 PP

2: /cgn2 6/ptodata/2/pubpna/USO6 NI

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4: /cgn2 6/ptodata/2/pubpna/USO6 NI

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12182.041 Million cell updates/sec
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: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/USO8_REW_PUB.seq:*
: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
: /cgn2_6/ptodata/2/pubpna/USO9B_PUBCOMB.seq:*
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  3 US-10-271-416-1

US-10-380-124-10

11 US-09-984-429-513

12 US-10-027-632-181221

US-10-027-632-181221

US-10-027-632-115440

US-10-027-632-115440

US-10-027-632-17813

US-10-027-632-17813

US-10-027-632-17813

US-10-027-632-17813

US-10-424-693-3

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Sequence 1, Appli
Sequence 513, Appl
Sequence 513, App
Sequence 181221,
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Sequence 115440,
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Sequence 17813, A
Sequence 17813, A
Sequence 17813, A
Sequence 3, Appli
Sequence 8, Appli
Sequence 8, Appli
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US-10-271-416-1/c
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Best Local Similarity 73.3%;
Matches 264; Conservative
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Publication No. US20040043021A1
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ALIGNMENTS

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GENERAL LEFORMANCE.

APPLICANT: Keith, Tim
APPLICANT: Little, Randall D.
APPLICANT: Untile, Randall D.
APPLICANT: Una Ecrdewegh, Paul
APPLICANT: Dupuis, Josee
APPLICANT: Dupuis, Josee
APPLICANT: Dupuis, Josee
TITLE OF INVENTION: NYCLEOFILDE AND ANINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4045
CURRENT APPLICATION NUMBER: US/10/271,416
CURRENT APPLICATION NUMBER: 60/328,424
PRIOR APPLICATION NUMBER: 60/328,424
PRIOR FILING DATE: 2001-10-11
PRIOR APPLICATION NUMBER: 50/328,424
PRIOR FILING DATE: 2001-10-11
SEQ ID NO 1
SEQ ID NO 1
SEQ ID NO 1
ORGANISM: Homo sapien
US-10-271-416-1
8
  155945 GAGGATTGCTTAAGCCCAGGAGTTTGAGACCAGCCTGGGCAACATGGTGAAACCCCATGT
                                                                                                 156005 AATCTCGTGGGGTGCGGTAGCTCACACCTGTAATCCCAGCAGCTTGGGAGGCCAAGGTGG
                                3339 GAGGATAGCTTGAGTCCAGCAGTTTGAGACCAGTCAGGGCAACACACAGCAGAGACCCCATAT
                                                                                                                               3279 AAAATAGATGAGTGTGGTGGCTCATGCCTGTAATCCCCAACACTTTGGGAAGCCGGGTCGG
                                                                                                                                                                                                      Score 196; DB 13; Length 304905; Pred. No. 4.2e-30; 0; Mismatches 95; Indels 1;
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155886
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RESULT 3
US-09-984-429-513
; Sequence 513, Applicat:
; Publication No. US2004
; Publication No. HORNATION:
; GENERAL INFORMATION:
; APPLICANT: Rosen et a
; ATITLE OF INVENTION: 5
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US-10-380-124-10
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; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: Isis Pharmaceuticals, Inc.
APPLICANT: Brett P. Monia
APPLICANT: Susan M. Freier
TITLS OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
ETLE REFERENCE: RIS-0156
CURRENT APPLICATION NUMBER: US/10/380,124
CURRENT FILING DATE: 2003-03-10
NUMBER OF SEQ ID NOS: 90
SEQ ID NO 10
LENGTH: 8133
TYPE: NUMBER: 013
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Best Local Similarity 74.6%;
Matches 249; Conservative
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Publication No. US20040053874A1
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                                                                                                                                                                                                                                                                                                                                                                                                                             TGAGGCTGCAGTGATCCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAA 3562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                АТАРАТАЛАТАЛАЛАЛАСТІТТАЛАЛАЛАСАЛАЛАТТАЛІТЛАЛІТТІЛАЛАЛАСЛІСА 3637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAAGCTGTCTCAAAAATA 3577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACCTGTAGTCTCAGCTACTCGGGAGGCTGAGGCAAGAGAGTCACCTGAGCCTGGAAGTT
                                                                                                              Application US/09984429
|o. US20040010132A1
                                53.
                                Human Secreted Proteins
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Pred. No. 3.4e-29;
0; Mismatches 84;
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RESULT 4
US-10-027-632-181221/c
Sequence 181221, Application US/10027632
; Sequence 181221, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
GENERAL INFORMATION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FITILE OF INVENTION NUMBER: US/10/027,632
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT APPLICATION NUMBER: US 60/218,006
pRIOR APPLICATION NUMBER: US 60/218,006
pRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-07-12
; PRIOR FILING DATE: 2000-04-20
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CUPRRENT APPLICATION NUMBER: US/09/984,429
CURRENT FILING DATE: 2001-10-30
PRIOR APPLICATION NUMBER: 60/244.591
PRIOR FILING DATE: 2000-11-01
PRIOR APPLICATION NUMBER: 09/288,143
PRIOR FILING DATE: 1999-04-08
PRIOR RELICATION NUMBER: PCT/US98/Z1142
PRIOR APPLICATION NUMBER: PCT/US98/Z1142
PRIOR APPLICATION NUMBER: 60/061,463
PRIOR APPLICATION NUMBER: 60/061,529
PRIOR APPLICATION NUMBER: 60/071,498
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,527
PRIOR FILING DATE: 1997-10-09
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PRIOR APPLICATION NUMBER: 60/061,527
PRIOR FILING DATE: 1997-10-09
PRIOR APPLICATION NUMBER: 60/061,536
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PRIOR FILING DATE: 1997-10-09
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Query Match
Best Local Similarity 76.1%; Pred. No. 1.2e-28;
Matches 242; Conservative 0; Mismatches 75;
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FITTLE OF INVENTION.

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRION APPLICATION NUMBER: US 60/218,006

PRIOR PELING DATE: 2000-07-12

PRIOR PPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23
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; TYPE: DNA
; ORGANISM: Human
US-10-027-632-181221
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US-10-027-632-181221/c
US-10-027-632
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 181221
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OR FILING DATE: 2000-02-24
OR APPLICATION NUMBER: US 60/167,363
OR FILING DATE: 1999-11-23
OR APPLICATION NUMBER: US 60/156,358
OR FILING DATE: 1999-09-28
OR APPLICATION NUMBER: US 60/146,002
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71.6%;
60/156,358
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Pred. No. 2.1e-29;
0; Mismatches 104;
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PILE REFERENCE 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT EILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-20
PRIOR FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR DATE: 1999-08-09
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; ORGANISM: Human
US-10-027-632-181221
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PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 181221
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 6C/218,0C6
PRIOR FILING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 6C/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 6C/193,483
PRIOR APPLICATION NUMBER: US 6C/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 6C/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 6C/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 6C/167,363
PRIOR APPLICATION NUMBER: US 6C/166,358
PRIOR APPLICATION NUMBER: US 6C/166,002
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 115440
LENGTH: 3287
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US-10-027-632-115440
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US-10-027-632-115440/c
                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-115440
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Exublication No. US20030204075A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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Best Local Similarity 76.3
Matches 254; Conservative
                                                                             Query Match
Best Local Similarity
Matches 254; Conserv
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                      3265 TTAAATTITITAAAAAATAGATGAGTGTGGGTGGGTGATGCGTGAATCCCAACACTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTGTAGTCCAAGCTACACAGGAAGCTGAGGCAGAAGGATCACTTGAGCCCAGGAGGTT 3504
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TITACITTITAATAAAGGCAGCTGGGTGCAGTGGCTCACACCTGTAATCCCAGCACTTTG
                                                                             Conservative
                                                                                             3.18;
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                                                                        Score 185.4; DB 16; Pred. No. 6.1e-29; 0; Mismatches 76;
                                                                             Indels
                                                                                                               Length 3287
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APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Movel Compositions and Met
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 808
LENGTH: 47903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 3.1%; Score 182.6; DB 17; Length 47903; Best Local Similarity 73.3%; Pred. No. 1.1e-27; Matches 247; Conservative 0; Mismatches 89; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              41168 AAATAAGCCAGGTGCTATGGTTCACGTCTACAACCCCAGCACTTTGGGAAGCTGACGCAG 41227
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                          ATAAATAAATAAAAATAACTTTTAAAAAAACAAAAATT
                                                                                                   CCATGAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAAGCTGTCTCAAAAATA 3577
                                                                                                                                                                                CTACACAGGAAGCTGAGGCAGAAGGATCACTTGAGGCCCAGGAGGTTGAGGCTGCAGTGAT 3518
                                                                                                                                                                                                                                                                                                                  GAGGATTGCTTGAGCCCAGGAATTTGAGACCAGCCTGGGCAACACAGTGAGACCTCATCT 41287
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                                                                                                                                                        TCACTTGGGAGGCTGAGGGAGGATCGCTTGAGTCTGAGAGGTTGAAGCTGCAATGAG 41407
                                                                                                                                                                                                                                   CTATTAAAAAAAAAAAAAAAAATTAGCCTGGGGTGGTGGCCCACACCTATGGTCCCAG 41347
                                                                                                                                                                                                                                                                         СТАВАВАВАСЕВИАСЕВИАСТВОСТВОСТВОСТСЯССТВО В 3458
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AAAAATAAATAAATAAAATTCTAAATAAATAAAACT 4150
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RESULT 9 US-10-027-632-17813; Ag

Application US/10027632

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CURRENT EILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 2000-03-29
PRIOR PELLING DATE: 1900-03-24
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-11-23
PRIOR PELLING DATE: 1999-09-28
PRIOR PELLING DATE: 1999-09-8
PRIOR PELLING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOPTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 17813
TYPE: DANA
RESULT 10
US-10-027-632-17813
; Sequence 17813, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single ?
TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
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; ORGANISM: Human
US-10-027-632-17813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 266;
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
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                                                                                                                                                                                                                                                                                                                               АЛАТААТААЛТААЛТАААЛТААСТІТТАЛАЛААСАЛАЛАТТАЛІТТАЛАТТІТАЛАЛАСА 3632
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-24
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR PILING DATE: 1000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 17813
LENGTH: 736
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Best Local S
Matches 266
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ORGANISM: Human
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al Similarity 68.2%;
266; Conservative
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TAAGTGAAAAGTAATGTCTGCAGAGCGCTT
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                                                                                          AAAAAAAAAAAAAAAATGAAAATGATAGTCTCAACCTCTTGGGATATGGGGGAGAGA
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504
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WESULT 11

US-09-964-469-3

US-09-964-469-3

Sequence 3, Application US/09964469

PATENT NO. US20020034803A1

GENERAL IMPORMATION:

GENERAL IMPORMATION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC

TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CL000636DIV

CURRENT APPLICATION NUMBER: US/09/964,469

CURRENT APPLICATION NUMBER: 60/208,331

PRIOR APPLICATION NUMBER: 60/208,331

PRIOR APPLICATION NUMBER: 09/738,894

PRIOR APPLICATION NUMBER: 09/738,894

PRIOR FILING DATE: 2000-12-18

MUMBER OF SEQ ID NOS: 4
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US-10-425-962-3
Sequence 3, Application US/10425962
Publication No. US20030180786A1
GENERAL INFORMATION:
APPLICANT: GUEGLER, KAY1 et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CL000636DIV2
CURRENT APPLICATION NUMBER: US/10/425,962
CURRENT APPLICATION NUMBER: US/10/425,962
CURRENT APPLICATION NUMBER: 09/984,469
PRIOR APPLICATION NUMBER: 09/984,469
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR APPLICATION NUMBER: 09/738,894
PRIOR FILLING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: 60/208,331
PRIOR FILLING DATE: 2000-104-01
SEQ ID NO 3
LENGTHARE: FastESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTHARE: PastESEQ for Windows Version 4.0
CRGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(36651)
COTHER INFORMATION: n = A,T,C or G
US-10-425-962-3
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SEQ ID NO 3
LENGTH: 36651
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Best Local Similarity 76.6%;
Matches 249; Conservative
Query Match
Best Local Similarity
Matches 249; Conserv
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NAME/KEY: misc_feature
LOCATION: (1)...(36651)
OTHER INFORMATION: n = A,T,C
-09-964-469-3
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  3.1%;
ilarity 76.6%;
Conservative
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Score 182.2; DB 15;
Pred. No. 1.2e-27;
0; Mismatches 73;
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    Indels
                                   Length 36651;

    Gape

    Gaps
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US-10-364-505-8/C
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Publication No. US20030219787A1

GENERAL INFORMATION:

APPLICANT: Kere, Juha
APPLICANT: Mo. US20030219787A101a-Hemmi, Jeana
APPLICANT: No. US20030219787A101a-Hemmi, Jeana
APPLICANT: Kaminen, Nina
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
APPLICANT: Kaminen, Nina
TITLE OF INVENTION UNMERR: US/10/364,505

CURRENT APPLICATION UNMERR: US/10/364,505

CURRENT FILING DATE: 2003-02-12

NUMBER OF SEQ ID NOS: 13

SOCTUMER: Deferit Ver. 2 1
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SEQ ID NO 8
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Best Local Similarity
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                                                                                                      AAAAACAAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTAC 3462
                                                                                                                                                                                             ATAGCTTGAGTCCAGCAGTTTGAGACCCAGTCAGGGCAACACAGCAGAGCACCCCATATCTAA 3402
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TTGGGAGGCTGAGGCGGGAGAATTGCTTGAACCAGGGAGGCAGAGCTTGCAGAGAGCCGA 16840
                            ACAGGAAGCTGAAGGAAGGATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCAT 3522
                                                                                                                                                                   ATCACCTGAAGTCAGGATTTTGAGACCAGCCTGGCCAACATGGCGAAACCCCCGTCTCTAC 16958
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RESULT 14
US-10-681-199-8/c
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RESULT 15
US-09-901-152-3
; Sequence 3, Application US/09901152
; Publication No. US20030022824Al
; GENERAL INFORMATION:
; APPLICANT: HU, Song et al.
; TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
; TITLE OF INVENTION: USES THEREOF
; TITLE OF INVENTION: USES THEREOF
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publication No. US20040138441A1
GENERAL IMPORMATION:
APPLICANT: KERE, Juha
TITLE OF INVENTION: NOVEL HUMAN GENE FUNCTIONALLY RELATED TO DYSLEXIA
FILE REFERENCE: 0933-0214P
CURRENT APPLICATION NUMBER: US/10/681,199
CURRENT FILING DATE: 2003-10-09
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity 68.4
Matches 281; Conservative
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LENGTH: 50000
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ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: human DYXC1 chromosomal gene region, nucleotides
OTHER INFORMATION: 100001-150000
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Search completed: September 27, 2004, 19:08:45 Job time: 2481 secs

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FILE REFERENCE: CL001248
CURRENT APPLICATION NUMBER: US/09/901,152
CURRENT FILING DATE: 2001-07-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
SEQ ID NO 3
LENGTH: 58985
TYPE: DNA
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LOCATION: (1)...(58985)
OTHER INFORMATION: n =
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Best Local Similarity 70.8%;
Matches 271; Conservative
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                      3603 AMAACAAMAATTAATTAAATTTT 3625
                                                                                                                     ATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACGCGGCTGCTACACT-CAG
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GÁTGAÁGCÁTTGÁÁTGÁGGTATT
                                                 TAGCCGAGCGTGGTGCATGCCTATAATCTCAGCTACTCGTGAAGCTGAGGCAGGAGA
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Pred. No. 2.8e-27;
0; Mismatches 105;
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Minimum DB seq length: 0
Maximum DB seq length: 200000000
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Perfect score:
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ALIGNMENTS

RESULT 1

AAF25905 standard; DNA; 5960

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Tumor suppressor; p51; cell death; cell proliferation; cancer;
cytostatic; gene therapy; screening; ds.
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                                                                                                             New DNA sequences encoding the human p51 promoter domain for screening for compounds that modify p51 promoter activity and for diagnosing and
                                                                                                                                      WPI; 2001-112452/12.
                                                                                                                                                     Sakai T, Kagaya S,
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This invention describes novel DNA sequences (I) encoding the human p51 promoter domain (which may include the 5'-untranslated sequence) or derived from it by addition, deletion and/or substitution of one or more bases. The invention also describes (1) expression plasmids including (I); (2) host cells transformed by (1); (3) DNA probes binding to all or pert of (I); (4) cloning (I) using (3); (5) DNA (and RNA corresponding to it inhibiting the expression of p51, which includes the antisense sequence of (I); (6) screening compounds for their ability to modify p51 promoter activity, by observing their effect on cells transformed by (I); (7) compounds identified by (6); and (8) drug compositions containing

Claim 1(4); Page 35-38; 60pp; Japanese.

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to screen for compounds corresponding to it are and the identified compe cancer 1175 G; 1824 T; 0 U; 0 O; e 5960; DB 5; Length 5; NO. 0; O Indels smatches O; Indels	(7). The products of the invention have cytostatic activity and can be
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 AMAGTICCAGGITGCTGAMATTAMACTICTGATGCCATTICATGCCAGCATCCAATCACGACA
                                                          TACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGACACTCATCAGCTCAGTTCAGTTACA
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AAF25915 standard; DNA; 13940 BP

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(first entry)

Tumor suppressor; p51; cell death; cell proliferation; cancer; cytostatic; gene therapy; screening; ds.

28-JUN-2000; 2000WO-JP004261.

99JP-00183195

(NIPK) NIPPON KAYAKU KK. (SAKA/) SAKAI T.

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Kagaya

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This invention describes novel DNA sequences (I) encoding the human p51 cc promoter domain (which may include the 5' untranslated sequence) or cc derived from it by addition, deletion and/or substitution of one or more cbases. The invention also describes (I) expression plasmids including (I) cc; (2) host cells transformed by (1); (3) DNA probes binding to all or cc pert of (I); (4) cloning (I) using (3); (5) DNA (and RNA corresponding to cell inhibiting the expression of p51, which includes the antisense cc sequence of (I); (6) screening compounds for their ability to modify p51 promoter activity, by observing their effect on cells transformed by (I); (7) compounds identified by (6); and (8) drug compositions containing cc (7). The products of the invention have cytostatic activity and can be composited that modify considered to gene therapy. (I) is used to screen for compounds that modify cpi promoter activity, (I) and RNA corresponding to it are used to confide the expression of p51. (I) and the identified compounds are used corresponding to it are used to confide the diagnosis and treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New DNA sequences encoding the human p51 promoter domain for screening for compounds that modify p51 promoter activity and for diagnosing and treating cancer.
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Local Similarity 99.3%;
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AAF25904 standard; DNA; 5676 В₽

19-APR-2001 (first entry)

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Human tumor suppressor gene p51 promoter associated DNA Ħ

Tumor suppressor; p51; cell death; cell proliferation; cancer; cytostatic; gene therapy; screening; ds.

WO200100818-A1

04-JAN-2001

28-JUN-2000; 2000WO-JP004261

99JP-00183195

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CC This invention describes novel DNA sequences (I) encoding the human p51 CC promoter domain (which may include the 5'-untranslated sequence) or CC derived from it by addition, deletion and/or substitution of one or more CC hases. The invention also describes (1) expression plasmids including (I) (; (2) host cells transformed by (I); (3) DNA probes binding to all or CC (i); (4) cloning (I) using (3); (5) DNA (and RNA) corresponding to CC (ii) inhibiting the expression of p51, which includes the antisense CC sequence of (I); (6) screening compounds for their ability to modify p51 (7) compounds identified by (6); and (8) drug compositions containing CC (7). The products of the invention have cytostatic activity and can be used for gene therapy. (I) is used to screen for compounds that modify (251 promoter activity. (I) and RNA corresponding to it are used to inhibit the expression of p51. (I) and the identified compounds are used to for the diagnosis and treatment of cancer
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Best Local Similarity
Matches 5676; Conserva
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3901 GCCTCXGGGGCXGATTAXAGCTTCGGGCTTGGACCTGGACTTCAACTCCAACCTTCCACCTTCACCTTCACCTACCACATACCACAAAACCCAAAAACCCAAAAACCCAAAAACCCAAAA	. ફ	901 GCCTCACGGGCACATTAAAACTTGAGAAGCTCTGCACTAGAAATCTTCACTCCACCTTTC 396
1911 ATTATANATIONATION CONTROGRED CONCOUNTED ANTICATION TITTANATION ADDITIONATION AND CONTROGRED AND CONCOUNTED ANTICATION TO ANTICATION AND CONTROL	2 0	901 GCCTCACGGGCACATTAAAACTTGAGAAGCTCTGCACTAGAAATCTTCACTCCACCTTTC 396
4021 CCTTCTATTINGGTCATCATATTTOCTANTAGCAGGAMGAAAGCCAAACTCTTTAACT 4081 CCTTCTATTINGGTCATCATATTTOCTANTAGCAGGAMGAAAGCCAAACTCTTTAACT 4081 CCAATTAACAAATCTATAATTAATTAGTTAAGCAGCAAACTCTTCACATTTTG 419 CCAATTAACAAATCTATAATTAATTAGTTAAGCAGCAACTCTTCCCTTTAAGTTTAACATTTTG 419 CCACAATTAACAAATCTATAATTATTAGTTTAAGCAATCTCCCTTTAAGTTTAACATTTTG 411 TGAAGCAAGCTGTTTGATTTGACTTTGACTTTAAGTTTACAATTTTG 411 TGAAGCAAGCTGTTTGATTTGACTTTGACATTTTGATTTTACAATTTTGAATTTTCACAATT 411 TGAAGCAAGCTGTTTGATTTGACTTGACAGCAACCAACTCACTTTAAGTTTAAATACATTTTGAT 412 CACAATTTACTGACGCCTCTCGGCCTAAGCAAACAAATTATTTTATGAAACAAATTTTTATGAATTTTCACAATT 413 TGAACTTACTTACAGGAAAATGTCAAATTTCTCTCTAAAAGAAATAATTTTTATGAATTTTCCCAAATTTTAAGATTTTAAGATTTTAAGATTTTTAAGATTTTTAAATAAT	유 왕	961 ATTATAAATGGAATCACTTGGGCTGTGGTCACAGGAAATTGATTATTTTTAATTTCAGAA 402
101 CANTIDACAATCINTALTIANTIGCTANGAGGAAGAACCAACCCTTRACTTTIACT 430 CCANTIDACAACCCTATATTACTATATATATATATATATATATATA	\$ \$	021 CCTTCTATTTAGGTCATCTATATTTGCTAATAGCAGGGAAGGAA
4081 CCANTINACAMATCHATHATTHATTHATCHATCANTTTALAGGGCANTTTALAGGGCANA 4141 TGGAGCAGCTGTTTGGATTTGGCTGGGGCTCAGGGCCGGCC	Ş ;	081 GCAATTAACAAATCTATAATTAATTAATTAAGCAATCTTAAGCATTTAAGCATTTAAGCATTTAAGCATTTAAGCATTTAAGCATTAAGCATTAAGCATTAAGCAATCTAAGCAATCTTAAGCATTAAGCATTAAGCATTTAAGCATTTAAGCAATCTAAGCAATCTAAGCAATCTAAGCAATCTAAGCAATCTAAGCAAGC
4141 TGGAGCAGCTGTTTGATTTGGCTGGGCCTCAGGCCGGCCTGTTTGTGATTTCACAATT	Db !	081 GCARTTAACAANICTATAATTAATTAAGTAAAGCAATCTTCCCTTTAAGTTTTACATTTTG 414
111 TGGGCAGCTCCACTTTCATTTGGCTGCGCCTCAGGAAGGA	i S	141 TGGAGCAAGCTGTTTGATTTCGCTGGGGCTCAGGCCTGGTTTGTGAATTTCACAATT 420
4201 CACAGATSTTAGCCGCTCTCGGCTTAAGGAAGGAAGGAAGGAAGGAAG	, 5	141 TGSAGCAAGCTGTTTGATTTGGCTGGGGCTCAGGCCGGCCTGTTTGTGAATTTCACAATT 420
4261 TCTCCCTTCCATCCTGGCTGAAGCAACAAATAAATATTTTTATGAAACACATTTTGAGT 4321 TAGATTTACTTACAGGGAAATGTCAAATTTTCTCTGAAAGGGCTTTAGATTGAACACATTTTCAGT 4321 TAGATTTACTTACAGGGAAATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTGACAAC 4321 TAGATTTACTTACAGGGAAATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTCACAAC 4321 TAGATTTACTTACAGGGAAATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTCACAAC 4321 TAGATTTACTTACAGGGAAATGTCAAATTTCTCTGAAAGGGCTTTAGATTGTCTCACAAC 4321 TAGATTTACTTACAGGGAAATGTCACAATTTACAGGTGTTCCTGTGACTAGGGGGTGAAAGGA 4321 TAGATTTACTTACAGGGAAATTACAGGTGTCTCTGTACAAAGGGA 4321 TTGGACTTCACTGATGTCACCCTATTTACAGGTGTCTCTGTCACTAAGGGA 4321 TTGGACTTCACTGATTACAGCCCTTACATTACAGGAAGTGGTTTTTTTT	₽ 5	201 CACAGA ISTINGC CECTUTOGGCTNAGTNAAGGAAGAGAGATGTCAAGTTTTAAATAGCT 426 []
4261 TCTCCCTTCCATCCTGGCTGAAGCAATAAATATTTTATCAGGCATTTAAGAATAAATA	Ş	261 TCTCCCTTCCATCCTGGCTGAAGCAAACAAATAAAATATTTTTATGAAACACATTTTGAGT 432
4321 TAGATTTACTGACAGGGAAATGCCAAAGGGCTTTAGAGTGCTCTACAAC 4381 TTTGACATCTACTGACGGGAATGCCAAATTCCTCTAAAAGGGCTTTAGATTCTCTCAAAT 4381 TTTGACATCTACTGATGTCACCTATTTACAGGTTGTCCTGTGACTAGGGGGTGAAGGGA 4441 AGATGTGACTCACCTATTTACAGGTTTACAGGTTTACAGAGTGGTTTTTTCCCCCTG 4501 TTTGACATCTCACCATGTTAGTGACCGTTAGAATACACAGAGTGGTTTTTTTCCCCCTG 4501 TTTGACATCTCACCATGTTAGTGACCGTTAGAATACACAGAGTGGTTTTTTTT	문	61 TCTCCCTTCCATCCTGGCTGAAGCAACAAATAAAATATTTTTTATGAAACACATTTTGGGT 432
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4381 TITGACATCIACTGATGTCACCTATTTACACATATATATATATATATATA	Ş	81 TTTGACATCTGATGTCACCTATTTACAGGTGTGTCTCTGACTAGGGGGTGAAGGGA 444
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4501 TTGGAGTCTAACTGACGTTCTGAATCATATTCATTCAATTCCAAATCCACAAA 456	D CY	41 AGATGTGAACTCACCATGTTAGTGACCGTTAGATACACAGAGTGGTTTTTTTCCCCCTG 450 41 AGATGTGAACTCACCATGTTAGTGACCGTTAGATACACAGAGTGGTTTTTTTT
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4561 ACCAGGATAAGTITACAGCCCATATTCAGAAAGAATAAATTATTTTTGTGTGTAGAACTT 4561 ACCAGGATAAGTITACAGCCCATATTCAGAAAGAAATAAATTATTTTTTTTTT	? ?	501 10000010141001444001101444011014ATTTCATTCAATTTCAATTCCACAAA 456
4621 TCCTGATAITACACTCAITTGGGAATAITATGAACAATTTTAITGGTTTCCTTTCGAAGTAG 468	ਲੋਂ ਵ	561 ACCAGGATAAGTITACAGCCCATATTCAGAAAGGAAATAAATTATTTTTGTGTGTAGACTT 462
4621 ICCTGATNTIACACTGATTTGGGAATATATATGAACAATTTTATGGTTTGCTTTCGGAAGTAG 4681 GTCAAGCAAAACCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAACAGCAAAAAA	* *	621 TCCTGATATTACACTGATTTGGGAATATATGAACAATTTTATGGTTTCCTTTCGAAGTAG 468
4681 TTACTATATTATATATATATATATATACTCCATGCATCTTGAGGTAGGT	? ;	681 GTCARGTGARARACHARIAGAARACHARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARIAGAARACHARACHARIAGAARACHARIAGAARACHARIAGAAARACHARIAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
4741 CCGACTGAGAGATTAÀAATAAACTAGAATATTTTATTAACAGGCAATTTGAAATAATTT 480	B	681 GTCAAGTCAAAGCAAAAACCAAAAACAGCAAAAACTGTAAGACATAAAGAATAGAGTGGAG 474
4/11 CUGACTUAGAGATTAAAATAAACTAGAATATTTTTATTAACAGGCAATTTGAAATAATTT 480 4801 GTGCACTTCAGAATATTCCTACCAATAATATTATTACCAATTTTAATATCTTTAAGAAAA 486 4801 GTGCACTTCAGAATATTCTACCAATAATATTATTTCCAATTTTAATATCTTTAAGAAAA 486 4801 GTGCACTTCAGAATATTCTAACATAATATTATTTCCAATTTTAATATCTTTAAGAAAA 486 4861 TTACTATTATTATATGTAAGTACATGTGCATGTGTTTGAGGTAGGATATTTAACTCAATAA 492 4861 TTACTATATTATATGTAAGTACATGTGCATGTTTGAGGTAGGATATTTAACTCAATAA 492	\$ Q	741 CCGACTGAGAGATTAAAATAAACTAGAATATTTTTTTAATGAGGGAATTTGAAATAATTT 480
4801 GTGCACTTCAGAATATTCTACCATTATTATTTCCAATTTTAATACTCTATAAGAAA 490 TTACTATATTATTATATGTAAGTACATGTGCATGTGTTTGAGGATATTTAACTCTCAATAA 491 HILLIHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	₹ 8	901 GTGCACTTTCAGAATTATTTCTAGAATAATTATTTTTTTT
4861 TTACTATATTATATGTAAGTACATGTGCATGTGTTTGAGGTAGGATATTTAACTCAATAA 492	ў	801 GTGCACTTCAGAATATTCTACAATAATATATTATCCAATTTTAATATCTTTAAGAAAA 486
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LAGGIATITGIGIATAITITATAIATAGITCTCCGT 5676	TGTCTGATAGCATTTGACCCTATTGCTTTTAGCCTCCCGGCTTTATATCTATATATA	TCAAGAAACGCTCCGCCTCTTGCAAATATGTATGAAGGAGAGAGA	GCTGGTAAGAATCGAGTGTTTATGAAGTTTTAGTCAATGATGAATCTCATTGGCTAAAA 5520 	TACGTCAAGGACTCTGAAGCCGTGAGAGAGGGGGGAAGAACAACAGTAGAGAGGAGGATGCCCA 5460 	1 GAGATCAGAAGTTCAGAGATGCCTCCAGCTCCAAATTGCCAACAACAAGTGTGGCTACTA 5400 	1 AAAGTCCAGGCTGCAGAATTAAACTCTGATGCCATTCATGCCAGCATCCAATCACGACA 5340 	1 TACAAGGAAGTGTTATGTAGCTGGAGCAGGGTGGACACTCATCAGCTCAGTTCAGTTACA 5280 	1 ACAAAACATTTTAGCCCCAGAAATAGTCACAGAGATCCACAATCAAACCAGTATCCAGA 5220	1 CGGGGAGGGAGATAGATGAAAAAAAAAAAAAAAAAAATTCCCTAAGCAGCTCT 5160 	1 GTCTTTGCTATTTGAGATTGTGACCACAACAGGCGGTTGGCTGAAAGGGAAACTGAACGG 5100 	1 CTTTCTCTTAGCTGAGAGGAAGAGTGAGTTCTAAGTTAAATATAATCAAGGAATTTCCCT 5040	1 AGGITATITICITITATICGGGTCAGGCAAAGCTICTAAGGGGATGTGAAAGGGATATCT 4980

Human tumor suppressor gene p51 promoter associated RNA SEQ ID 4.

RESULT 4

AAP25907/c

ID AAP25907 standard; RNA; 5676 BP.

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AC AAP25907;

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DT 19-APR-2001 (first entry)

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DB Human tumor suppressor gene p51 pro

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CY

CY

Cytostatic; gene therapy; screening

XX

DS

Homo sapiens.

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PD 04-JAN-2001. Tumor suppressor; p51; cell death; cell proliferation; cancer; cytostatic; gene therapy; screening; ds.

28-JUN-2000; 2000WO-JP004261

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This invention describes novel DNA sequences (1) encoding the human p51 CC promoter domain (which may include the 5'-untranslated sequence) or CC derived from it by addition, deletion and/or substitution of one or more CC derived from it by addition, deletion and/or substitution of one or more CC bases. The invention also describes (1) expression plasmids including (1) (2) host cells transformed by (1); (3) DNA probes binding to all or CC pert of (1); (4) cloning (1) using (3); (5) DNA (and RNA corresponding to CC it) inhibiting the expression of p51, which includes the antisense CC sequence of (1); (6) screening compounds for their ability to modify p51 promoter activity, by observing their effect on cells transformed by (1); (7) compounds identified by (6); and (8) drug compositions containing CC (7). The products of the invention have cytostatic activity and can be CC used for gene therapy. (1) is used to screen for compounds that modify CC promoter activity. (1) and RNA corresponding to it are used to CC inhibit the expression of p51. (1) and the identified compounds are used CC for the diagnosis and treatment of cancer
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Matches 5676
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RBSULT 5
AAF25906/c
ID AAF25906 standard; DNA; 5676 BP.

XX AAF25906;
XX AAF25906;
XX DT 19-APR-2001 (first entry)
XX Tumor suppressor gene p51 promoter associated DNA SEQ ID XX Tumor suppressor; p51; cell death; cell proliferation; cancer; XX cytostatic; gene therapy; screening; ds.

XX OS Homo sapiens.

XX WO200100818-A1.

XX PD 04-JAN-2001.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel DNA sequences (I) encoding the human p51 promoter domain (which may include the 5'-untranslated sequence) or derived from it by addition, deletion and/or substitution of one or more bases. The invention also describes (I) expression plasmids including (I); (2) host cells transformed by (I); (3) DNA probes binding to all or pert of (I); (4) cloning (I) using (3); (5) DNA (and RNA corresponding to it) inhibiting the expression of p51, which includes the antisense sequence of (I); (6) screening compounds for their ability to modify p51 promoter activity, by observing their effect on cells transformed by (I); (7) compounds identified by (6); and (8) drug compositions containing (7). The products of the invention have cytostatic activity and can be used for gene therapy. (I) is used to screen for compounds that modify p51 promoter activity. (I) and RNA corresponding to it are used to inhibit the expression of p51. (I) and the identified compounds are used to for the diagnosis and treatment of cancer
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                                                         GTCAAGTCAAAGCAAAACCAAAAACAGCAAAAACTGTAAGACATAAAGAATAGAGTGGAG
                                                                                                                                                                                                                    TTGGAGTCTATCCTAACTGAGCTTCTGAATCATATTTCATTTCAATTTCCAAATCCACAAA 4560
                                                                                                                                                                                                                                                                                                                                                                                  TCTCCCTTCCATCCTGGCTGAAGCAACAAATAAAATATTTTTATGAAACACATTTTGAGT
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                                 GTGCACTICAGAATATTCTACAATAATATATTATTTCCAATTTTAATATCTTTAAGAAA 4860
                                                                                                                                      TCCTGATATTACACTGATTTGGAATATATGAACAATTTTATGGTTTCCTTTCGAAGTAG
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                                                           GCTGGTAAGAATCGAGTGTTTATGAAGTTTTAGTCAATTGATGATGAATCTCATTGGCTAAAA 5520
                  AAAGTCCAGGCTGCTGAAATTAAACTCTGATGCCATTCATGCCAGCATCCAATCACGACA 5340
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RESULT 6
ABX56555/c

ID ABX56555 standard; DNA; 118384 BP
XX ABX56555;
XX

DT 20-FEB-2003 (first entry)
XX

XX

PHUMAN autoimmune disease related;
XX

XW

PAT1; human; autoimmune disease;;
XX

XX

PAT1; human; autoimmune disease;;
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PAT1; human; Human autoimmune disease related protein PAT1 gene region

PAT1; human; autoimmune disease; psoriasis; type I diabetes; rheumatoid arthritis; cation-chloride transport; gene therapy; gene; ds.

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Matches 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New PATI genes and polypeptides, useful for diagnosing the presence or a susceptibility to, an autoimmune disease (e.g. psoriasis, type diabetes or rheumatoid arthritis), or screening agents for treating autoimmune diseases.
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05-APR-2001; 2001GB-00008589
05-APR-2001; 2001GB-00008590
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or treating, an autoimmune disease. This polynucleotide from the human PAT1 gene
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                                                                                                                                      CAGCTACTTGGGAAGCTGAGGTGGGAGGATCACTTGAACCCAGGAGGCGGAGGTTGTAGC 11440
                                                                                                                                                                                                                                                                                                                                                     TCTCTATTAAA -- AACACAAAACAAAATTAGCTGGGTGTGGTTGTACACGCCTGTAATCC
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Pred. No. 1.3e-26;
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Homo sapiens.

26-MAR-1999; 22-DEC-1999; W0200057903-A2. WPI; 2000-594630/56 P-PSDB; AAB39342. 22-MAR-2000; 2000WO-US007525 (HUMA-) HUMAN Ş Ruben SM, GENOME 99US-0126595P. 99US-0171549P. ູດ

New nucleic acid molecules encoding 48 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions used as food additives or preservatives.

Claim 1; Page 339-340; 395pp; English.

The polynucleotide sequences given in AAC74280 to AAC74327 encode the CC human secreted proteins given in AAB39357. AAB39358 to CAAB39400 represent human secreted polypeptide sequences and proteins CC hambologous to them, which are given in the exemplification of the present CC invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Examples of activities include: CC and cells the genes are expressed in. Examples of activities include: CC exprostatic, cardiant, vasotropic, cerebroprotective; mostropic; cerebroprotective; cardiaction in e.g. humans, mice, crabbits, goats, horses, cats, dogs, chickens or sheep. They can also used condition or susceptibility to a pathological condition or susceptibility to a pathological condition. Disorders which are disorders, cardiovascular cc disorders, infections caused by bacteria, viruses and fingly and ocular condition or prevent skin aging due to sunburn, to constitute or decrease storage capabilities, fat content, lipid, protein, components. AAC74271 to AAC74273 and AAB39309 represent sequences used in the activity of the present invention the exemplification of the present invention

Sequence 1384 BP; 443 A; 247 C; 254 G; 440 T; 0 U; 0 Other;

Query Match Best Local S Matches 277 3.2%;
al Similarity 71.9%;
277; Conservative ; Score 189.4; ; Pred. No. 4e-2 0; Mismatches 4e-26; DB 3; 101; Length 1384; 7; Gaps

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The invention comprises antisense oligonucleotides that are capable of inhibiting expression of the human clusterin gene. The antisense oligonucleotides of the invention are useful for inhibiting the expression of clusterin in cells. The antisense oligonucleotides are also useful for treating an animal with a disease or condition associated with clusterin (e.g. hypercholesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterolesterol
                                                                                                                                                                                                                                                                                                                                                      Novel antisense compound targeted to nucleic acid molecule encoding clusterin, useful for treating animal having disease associated with clusterin such as hyperlipidemic disorder, cardiovascular disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; antisense inhibition; antisense oligonucleotide; clusterin; hypercholesterolaemia; cardiovascular disorder; ds; hyperproliferative disorder; hyperlipidemic disorder.
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                                                                                                                                                                                                                                                                                    Example 15; Page 93-98; 125pp; English.
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                                                                                                           exon
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stic marker; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGAGGCCAAGGCGGGAGGATCATTTGAGGCCAGGAGTTTGAGACCAGCCTGGCCAAGAT 1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8133 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CACCTGTAGTCCAAGCTACACAGGAAGCTGAGCCAGAAGGATCACTTGAGCCCCAGGAGGT 3503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTAAAGAGGAAAAAAACTGAGCTGGGCATGGTGGCTCATGCCTGTGATGCCAGCACTTT
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Pred. No. 1.1e-25
0; Mismatches 8
                                                                                                                                                                                                                                                                                                                                                                                            TTYH2
                                                                                                                                                                                                                                                                                                                                                                                       protein'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2125 T;
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The invention relates to human tweety homologue 2 (TTYH2) polypeptide and polynucleotide sequence. TTYH2 is useful for producing an antigen-binding molecule that is immuno-interactive with the polypeptide. The agent is useful for manufacturing a medicament for restoring a normal level and/or
                                                                                                                                   New human tweety homolog 2 polypeptides and polynucleotides, useful for producing an antigen-binding molecule that is immuno-interactive with the polypeptide or as diagnostic markers for cancers.
                                                                                                                                                                                                                  WPI; 2003-129264/12.
P-PSDB; AAE34613.
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Matches 245;
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neurological disease; mental disorder: psychiatric illness;
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one or more
rs. The present
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exon

exon

exon

intron

exon

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intron

14-MAY-2002;

Claim

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The invention relates to an isolated or purified polynucleotide encoding a polypeptide (the wild-type form of which is involved in synaptogenesis) that includes at least one mutation associated with development of neurological disease and/or a predisposition to development of mental disorders or psychiatric illness. The polypeptide are used to screen for agents that modulate their activity. Also nucleic acid, polypeptide. The polypeptide of the screen for polypeptide specific antibodies, vectors containing he nucleic acid and host cells containing the vector, are useful as pharmaceuticals for treating mental and neurological disorders, specifically autism, Asperger syndrome, schizophrenia and attention deficit hyperactivity disorder. The wild-type forms of the nucleic acid and polypeptide can be used wild-type forms of the nucleic acid and polypeptide can be used to detect biochemical disorders that affect formation of synappes and to diagnose mental wild true halfs sequence corresponds to the genomic sequence of the buman wild true halfs sequence corresponds to the genomic sequence of the
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Gillberg C;
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                                                                                                                                                                                                                                       schizophrenia.
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(INSD ) INST PASTEUR.
(ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
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RESULT 11
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Best Local Sim
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                                                                                                                                                                                                                                                                            Human; kinase; G-protein coupled receptor kinase; tissue differentiation; chromosome 3; therapeutic; immune response; drug screening; enzyme; SNP; single nucleotide polymorphism; ds.
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Similarity 65.2%;
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             replace (3672,T)
/*tag= e
/standard_name= '
replace (3884,C)
/*tag= f
                                                                                                                            /product= "Human
2076. .2687
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2076. .33928
                                                                                                                                                                                                           replace (2022, T)
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   standard_name= "Single nucleotide polymorphism"
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Pred. No. 1.3e-24;
0; Mismatches 155;
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replace (9233, A)
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/*tag= m
  /standard_name= *
replace(20105,G)
/*tag= ae
/standard_name= '
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replace(7344,C)
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replace(5268,C)
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replace(15045,T)
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replace(14376. .
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replace(9747,M)
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replace(17482,G)
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replace(13884,C)
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replace(13721,T)
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replace(11635,A)
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   The invention relates to human kinase proteins that are related to G-
protein coupled receptor kinase subfamily. Human kinase gene is located
on chromosome 3. The kinase peptide and nucleic acid are useful in the
development of human therapeutic and diagnostic compositions. The peptide
is useful as a major target for drug action and development, and is
valuable to the field of pharmaceutical development to identify and
characterise modulators of the kinase. The proteins may also be used to
raise antibodies or to elicit an immune response, as a reagent in assays
designed to quantitatively determine levels of the protein in biological
fluids and as markers for tissues in which the corresponding protein is
preferentially expressed (either constitutively or at a particular stage
                                                                                                                                                       New isolated human kinase proteins and nucleic acids, target for drug action and development, particularly tmodulators of the kinase peptides.
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18-DEC-2000;
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replace(24278,A)
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replace(34983,A)
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replace(34821,G)
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Matches 249;
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New isolated, purified DYXC1 nucleic acid for studying brain processes, e.g. reading, phonological processing, rapid naming or verbal short-term memory, or for diagnosing dyslexia or assessing the predisposition to
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                                                                                                                                                                                                                                             LICENTIA LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAACAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGGAA 3469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGCTGTGACTCACGCCTGTAATCCCAACACTTTGGGAAGCCAAGGTGGGAGAATCCCCTT
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                                                                                                                                                                                   Taipale M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAAAACGAGAACAAAAACAAATAAT 11847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAAATAACTTTTAAAAAACAAAAAT 3613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CIGCTACACT-CAGICIGGGIGACAGIGCAAGAAGCIGICTCAAAAATAAATAAATAAATA 3588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            scrigagecaggaggarrectrigasceressastririgassecrecassrascerigareaca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 182.2; DB 6;
Pred. No. 1.4e-24;
0; Mismatches 73;
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                                                                                                                                                                                      Kaminen
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RESULT 13
ABZ59738
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Best Local S
Matches 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to a novel isolated human gene DXXC1 that is functionally related to dyslexia, more particularly it describes single nucleotide polymorphisms thought to prediapose an individual in to developing dyslexia. This is a neurological disorder with a genetic basis (DXXC1 has been isolated to chromosome 15g21), which manifests itself as a specific reading disability. Specifically, DXXC1 is can be useful in study of brain processes such as reading, phonological processing, rapid naming and verbal short-term memory. Accordingly, the present invention describes methods and materials for analysing allelic variations in the DXXC1 gene, and also provides DXXC1 as an antigen for the production of antibodies used in the diagnosis of dyslexia. This polynucleotide is the partial genomic sequence of the human DXXC1 chromosomal region (nucleotides 100001-150000) of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 49939 BP; 13786 A; 10910 C; 11127 G; 14116 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTTACAAAATATATATAATTATTACAAGAAAGTTATAGTTTCTTAATTTAAACAAGCAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAACAAAAAACAAACAAGCAAAAACATGGTAAAAATTCTAATTTTAAAATA 16729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              АТАЛАТАЛАЛАТАЛСТТТАЛАЛАЛАСЛАЛАЛТТАЛАТТТАЛАЛАЛАСА 3632
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Pred. No. 1.7e-24;
0; Mismatches 127
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Human; secreted protein; epidermal cancer; gene; ds.

growth

factor;

EGF;

chromosome

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Homo sapiens

variation variation

Location/Qualifiers
replace (548,A)
/*tag= a
/standard name= "Sin
replace (2201,A)

"Single

nucleotide polymorphism"

Human secreted protein genomic sequence SEQ

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            New isolated peptide, useful for treating a disease by a human secreted protein e.g. cancer.
                                                         WPI; 2003-210419/20
P-PSDB; ABP71736.
                                                                                                                                                                                                                                                            WO2003006481-A2
                                                                                                    Ketchum K,
                                                                                                                                   APPLERA CORP.
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replace(22575,G)
/*tag= 8
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'7778. .7909
/*tag= g
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/*tag= d
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/product= "human
/note= "contains
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replace(22425,G)
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21576. .21727
*tag= p_
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eplace(14860,G)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard name= "Single nucleotide polymorphism" eplace(16510,C)
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eplace(16060,G)
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                             condition mediated
RESULT 14
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XX ABZ22
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Best Local Sim
Matches 271;
                                                                                                                     Key
variation
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secreted protein genomic DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel human secreted protein that is related to the epidermal growth factor (EGF) superfamily. The activity of the protein of the invention may be described as cytostatic. The protein of the invention is useful for preparing a composition for diagnosing or treating a disease or condition mediated by human secreted proteins, including cancer. The gene encoding the protein of the invention may be found on human chromosome 22. The current sequence represents the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1 b; Fig 3; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 58985 BP; 13362 A; 14853 C; 15805 G;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                              AATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACC
GATGAAGCATTGAATGAGGTATT
                       AAAACAAAATTAATTAAATTT 3625
                                                            <u>ATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATGGCGCCACTGCACTCCAG</u>
                                                                                                                                                      ATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACGCGCTGCTACACT-CAG
                                                                                                                                                                                          TAGECGAGCGTGGTGCATGCCTATAATCTCAGCTACTCGTGAAGCTGAGGCAGGAGA
                                                                                                                                                                                                             TACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGGAAGCTGAGGCAGAAGG
                                                                                                                                                                                                                                                        AATCCCAGCACTTTGGGAGACCGAGGCAGGCAGATTACCTGAGGTCAAGAGTTTGAGACC
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
8524
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2.5e-24;
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Human; secreted protein; epidermal growth factor protein subfamily; epidermal growth factor; EGF; gene therapy; therapeutic; drug screening; biological activity; immune response; chromosome 22; SNP; gene; single nuclcotide polymorphism; ds.
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                              Human epidermal growth factor related secreted protein DNA SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABZ22654 standard; DNA; 143601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                        /standard name= "single nucleotide polymorphism
2076. 140828
                                                                                                                                                                              Location/Qualifiers replace(1277,A)
                 procein"
                                            /*tag= b
/product= "EGF protein subfamily related
"contains
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introns'
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(SNP)

variation	FT intron FT	exon	variation	-		vari	variation		_	Variation Value	FT CONTRACTOR			r r variation	FT FT variation	T Variation		r r variation	intron	r exon	r variation	variation	intron	
<pre>/number= 3 replace(25436,A) /*tag= 2</pre>	/number= 3 2535654132 /*tag= y	/*cag* w /standard_name= "; 2522725355 /*tag= x	≥ ï	년 .) i	s rd_name= " (21858,A)	/*tag= r /standard_name= "s replace(20858.G)	2	<u> </u>	replace(1/494,1) /*tag= 0 /standard name= "s	/*tag= er /number= 9		•	<pre>/*tag= 1 /standard_name= "s replace(14341,G)</pre>	Ŭ.	<pre>/*tag= j /standard_name= "g replace(13141,G)</pre>	i ard name: e (8334	<pre>/*tag= n /number= 2 replace(7034,A)</pre>	/"Lay= 9 /number= 2 619125226	ard_name= " .6190	<pre>/standard_name= "s replace(4814,C) /*tag= f</pre>	4260. e	21646058 /*tag= d /zumber= 1	/*tag= c /number= 1
		"sirgle nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism		single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	single nucleotide polymorphism	∘ "single nucleotide polymorphism .8335,G)			single nucleotide polymorphism	single nucleotide polymorphism			
		n (SNP) "	ı (SNP) "	n (SNP)"	" (GNS)	(SNP) "	a (SNP)"	n (SNP)"	(SNP) "	(SNP) "	•	ı (SNP) "	(SNP) *	(SNP)	(SNP)"	(SNP)"	1 (SNP)"			(SNP)"	(SNP) *			
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FT variation	FT variation FT	FT variation	FT variation	FT variation FT	FT variation	FT variation	FT variation	FT variation	FT variation	FT variation	FT variation	FT variation	FT variation	FT variation	FT variation FT	FT variation	FT variation FT	FT variation FT	FT variation FT	FT variation	FT variation FT		FT variation	FT variation
variation	variation I	variation x	variation r	/standard_name variation replace (44837, /*tag= at	variation :	variation replace (42	/ cay= ap /standard variation replace (40	variation replace (35620,	variation r	variation r	variation r	variation	variation	variation r	variation	variation	variation	variation r	variation	variation	variation r	/*tag= ab /standard_name=	/*tag= aa /standard_name= variation replace(25733.	variation
variation replace(52639,C) /*tag= ay /*stag= ay	<pre>variation replace(46514,Y) /*tag= ax /standard name= "single")</pre>	variation x	/standard_name= "single variation replace(4499544996,A) /*tag=_au	variation	/standar replace(/*tag=	variation /standar /*tag=	/".tag= /standar variation replace /*fag=	variation	variation replace	variation replace	variation replace	variation replace	/standar variation replace	/standamy /stand	/standard_name= "single variation replace(30219,C) /*tag= ai	variation /standamy /stag=	/standar variation replace /*tag=	/standard_name= "single replace(25984,C) /*tag= af	variation replace (25980,G) /*tag= ae	variation replace (25966, A)	variation replace(26583,C) /*tag= ac /standard_name=	/*tag= ab /standard_name=	variation	variation 1

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RESULT 15
AAS42041/c
ID AAS42041 standard; DNA; 26329 BP.
XX AAS42041;
AC AAS42041;
XX DE 17-DEC-2001 (first entry)
XX DE Genomic sequence #357 encoding nove
XX
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Best Local Sim
Matches 271;
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              Genomic sequence #357 encoding novel human enzyme polypeptide
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                                                                                                                                                                                                                                                                                                                        TACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGAGGAAGGCTGAGGCAGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAGGCTATAAACCTTTTAAAATTTTTTAAAAAAAAAAATAGATGAGTGTGGGTGGCTCATGCCTGT
                                                                                                                                                                     AAAACAAAATTAATTAAATTTT 3625
                                                                                                                                                                                                                        ATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACGCGCTGCTACACT-CAG
                                                                                                                                                                                                                                                                                                                                                                                                                             AATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTTGAGTCCAGCAGTTTGAGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                             GATGAAGCATTGAATGAGGTATT
                                                                                                                                                                                                      TAGCCGAGCGTGGTGCATGCCTATAATCTCAGCTACTCGTGAAGCTGAGGCAGGAGA
                                                                                                                                                                                                                                                                                                                                                         NATCCCAGCACTTTGGGAGACCGAGGCAGGCAGATTACCTGAGGTCAAGAGTTTGAGACC
                                                                                                                                                                                                                                                       ATCACTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATGGCGCCACTGCACTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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/number= 4
replace(56111,T)
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54668. .82032
/*tag= bc
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replace(52748. .52749,T)
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*tag= bh

/standard name= "single nucleotide
replace (63894,G)

/*tag= bi
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/*tag= be
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/*tag= bb
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replace(60650,A)
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Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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.8e-24;
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  14.JUL-2000

26.JUL-2000

26.JUL-2000

26.JUL-2000

14.AUG-2000

16.AUG-2000

22.AUG-2000

22.AUG-2000

23.AUG-2000

23.AUG-2000

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01.SEP-2000

06.SEP-2000

06.SEP-2000

06.SEP-2000

07.SEP-2000

08.SEP-2000

08.SEP-2000

09.SEP-2000

09.SEP-2000

14.SEP-2000

14.SEP-2000
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2000US-022526P

2000US-022547P

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2000US-0218390P.
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2000US-0225213P.
2000US-C225214P.
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21-SEP-2000;
21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
25-SEP-2000;
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2000US-0236327P.
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2000US-0241809P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the isolation of novel human enzyme colymeptides (ANUZ2915-ANUZ3914), and the cDNA and genomic sequences crowding them. The enzyme polymeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, clasmers related to prevention and/or prognosis of a wide range of cdiagnosis, treatment, prevention and/or prognosis of a wide range of cdisorders including hyperproliferative disorders (e.g. cancer), the composis, treatment, prevention and/or prognosis of a wide range of cdisorders including hyperproliferative disorders (e.g. cancer), the composis, treatment, prevention and/or prognosis of a wide range of cdisorders including hyperproliferative disorders (e.g. cancer), metabolic cdisorders (e.g. alsorders), and includent of ce.g. phenylketonuria), inflammatory disorders (e.g. asthma), cdisorders (e.g. asthroscelerosis), blood-related disorders (e.g. atheroscelerosis), blood-related disorders (e.g. haemophilia), reproductive disorders (e.g. infertility) and cliffication also be used in gene tharapy. ANA41685-ANA42102 represent CC invention can also be used in gene tharapy. ANA41685-ANA42102 represent CC invention which is the sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly cfrom WIPO at ftp.wipo.int/pub/published_pct_sequences
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Best Local S
Matches 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           00-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 26329 BP; 6954 A; 5487 C; 5702 G; 8186 T; 0 U; 0 Other;
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ALIGNMENTS

	PUBMED	JOURNAL	TITLE	AUTHORS		SOURCE ORGANISM	VERSION KEYWORDS	ACCESSION	LOCUS DEFINITION	RESULT 1
High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618	10449764 Contact: Mahairas GG, Wallace JC, Hood L	scanning the human genome Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999) 99180589	Hood, L. Sequence-tagged connectors: A sequence approach to mapping and	L (Dages I Co 523) Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	Homo sapiens (human) Homo sapiens	AQ168656.1 GI:3566331 GSS.	<pre>sapiens genomic clone Plate=3165 Col=16 Row-L, genomic survey sequence. A0168656</pre>	AQ168556 S23 bp DNA linear GSS 16-OCT-1998 HS 3165 B2_F08_T7 CIT Approved Human Genomic Sperm Library D Homo	

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Class: BAC ends
High quality sequence stop: 523
Location/Qualifiers
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Mus musculus (house mouse)

Mus musculus (house mouse)
                                                                                                     BY723946 FIXEN full-length enriched, adult male hypothalamus Mus musculus cDNA clone A230061P11 5', mRNA sequence.

BY723946 GI:27137063
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Similarity 90.6%;
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Email: jwallace@u.washington.edu
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
B-Coli DH10B"
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URL:http://genome.guec.riken.go.jp/
Adachi,J., Alzawa,K., Akimuza,T., Arakawa,T., Carninci,P.,
Adachi,J., Alzawa,K., Akimuza,T., Arakawa,T., Carninci,P.,
Adachi,J., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F.,
Fukuda,S., Hashizume,W., Hayashida,K., Mirata,M., Nakamura,K.,
Kondo,S., Konno,H., Koya,S., Miyazaki,A., Mirata,M., Nakamura,K.,
Kondo,S., Konno,H., Koya,S., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Saito,R., Sakazume,N.,
Sano,H., Sasaki,D., Sato,K., Shibats,K., Shiraki,T., Tagami,M.,
Takeda,Y., Maki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission

Computational Analysis of Full-Length Mouse CDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (200m)
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Re 10 (11), 1757-1711 (2000)
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Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SGC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Jag
                                                                                                                                                                                                                                                                                                                            prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp)
further details.
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="A230061P11"
                                                                                                                                                                                                                                                                ocation/Qualifiers
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JOURNAL MEDLINE PUBMED TITLE

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Query Match
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                                                                                                                                                                                                                                                                                                           CGTCAAGGACTCTGAAGCCGTGAGAGAGGGGGGAAGAACAACAGTAGAGAGGAGGATGCCCAGC 5462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCAGAAGTTCAGAGATGCCTCCCAGCTCCAAATTGCCCAACAACAAGTGTGGCTACTATA 5402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTCCAGGCTGCTGAAATTAAACTCTGATGCCATTCATGCCAGCATCCAATCACGACAGA 5342
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                                                                                                            AAATGAATTTTGAAACTTCACGGTGTGCCACCCTACAGTACTGCCCTGACCCTTACATCC
                                                                                                                                                                            GTATTTGTGTATATTTTATATATTAGTTCTCCGTTCGTTGATATCAAAGACAGTTGAAGG
                                                                                                                                                                                                                                         AAGAAACGCCCCGCCTCTTTGCAAATCTGAGTAAAGGGGGGAAGTGTCTAAACTTCTATG
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                                                            AGCGGTGAGTTTGAATGTGACATAACTTCTC 5793
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothalamus"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RIKEN full-length enriched, adult male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="adult
/lab_host="DH10B"
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Pred. No. 7.9e-45;
0; Mismatches 118;
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BG219090 288 bp r RST38843 Athereys RAGE Library Homo

mRNA 1 o sapiens

linear

EST 21-APR-2001 mRNA sequence.

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Best Local Sim
Matches 281;
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1 (bases 1 to 293)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Cfechbacher,J., Danzig,J. and Ducar,M.

Creation of genome-wide protein expression libraries using random activation of gene expression

Nat. Biotechnol. 19 (5), 440-445 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3201 Carnegie Ave,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Scott J. Cain
Athersys, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11329013
                                                                                                                                                                                                                                                                                                                                                                                        Similarity 99.6%;
                        GCAGTTTGAGACCAGTCAGGGCAACACACAGCAAGACCCCCATAT 3398
                                                                                         GGCTCATGCCTGTAATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTTGAGTCCA
                                                                                                                                                                 TATTTAAATACGTTAGGCTATAAACCTTTTAAATTTTTTAAAAAAATAGATGAGTGTGGT 3296
                                                                                                                                                                                                                                             AGTAACTTTAGGATTTTTAAATAACAACTATTGAAATCATGACATACGTTTAAATGATAT
                                                                                                                                                                                                                                                                                          GCAGTTTGAGACCAGTCAGGGCAACACACCAGCAAGACCCCCATAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l: scain@athersys.com
quality sequence stop:
   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db xref="taxon:9606"
/cell_line="HT1080"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression
/Inbraries using Random Activation of Gene Expression',
Mature Biotechmology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                   Score 280.4; DB 12; Pred. No. 1.3e-30; 0; Mismatches 1;
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o sapiens cDNA, mRNA sequence.
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3201 Carnegie Ave, (
Tel: 216 431 9900
Fax: 216 361 9596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McElligott, K., Boozer, S., Mays, R., Smith, E., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M.
Creation of genome-wide protein expression libraries using random activation of genome-wide protein expression libraries using random labeliance of genome-wide protein expression libraries using random activation of genome expression
              BG212753 277 bp mRNA 1
RST32248 Athersys RAGE Library Homo sapiens
BG212753 BG212753.1 GI:13734440
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                  TAACTTTAGGATTTTTAAATAACAACTATTGAAATCATGACATACGTTTAAATGATATTA 3238
                                                                                                                                                                                AGTTTGAGACCAGTCAGGGCAACACAGCCAAGACCC 3393
                                                                                                                                                                                                                            CTCATCCCTGTAATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTTGAGTCCAGC 3558
                                                                                                                                                                                                                                                                                                                                                          TAACTTTAGGATTTTTAAATAACAACTATTGAAATCATGACATACGTTTAAATGGTATTA
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Location/Qualifiers
sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Athersys RAGE Library"
/clone_See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression'
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
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98.2%;
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Pred. No. 1.1e-28;
0; Mismatches 5;
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                                                            EST 21-APR-2001 mRNA sequence.
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Best Local Sim
Matches 265;
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216 361 9596
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ORGANISM
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df132c05.yl Morton Fetal Cochlea Homo
IMAGE:2537481 5', mRNA sequence.
BI497128
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Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression nat. Biotechnol. 19 (5), 440-445 (2001)
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larity 98.1%;
Conservative
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/note="See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_line="HT1080"
                                                                                                                                GI:15336472
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Pred. No. 5.9e-28;
0; Mismatches 5;
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                             Euteleostomi;
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Best Local Similarity 68.68;
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Robertson,N.G., Khetarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening Genomics 23, 42-50 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequencing and analyses were performed by National Institute of Health Intramural Sequencing Center (NISC; see http://www.nisc.nih.gov)
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Plate: LLAN6320 row: F column: 10
Seq primer: MijRP1 reverse primer (ABI).
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Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 617 732 7980
Fax: 617 738 6996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Departments of Pathology and Obstetrics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Morton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genomics 23, 95130111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: ccmorton@bics.bwh.harvard.edu
                   GCTGAGGCAGAAGGATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACGCG
                                                                                                                                         ATAGA----AAAATTAGCTGGGCATGGTGGCGTGTGCCTGTAGTCCCAGCTACTCGGGAG
                                                                                                                                                              AAACAAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGGTCCAAGCTACACAGGAA 3469
                                                                                                                                                                                                            GAGCTCAGGAGTTCAAGACCACCCTGGGCAACACAGCGAGATACTATCTCTACAAAAAAA
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                                                                                                                                                                                                                                                                                                                  GTGTGGTGGCTCATGCCTGTAATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTT 3349
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2537481"
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Pred. No. 4.8e-17;
0; Mismatches 129;
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AUTHORS
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Best Local &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: CITBI-E1-2517A7,TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Butheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 64)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AQ275866 664 bp CITBI-E1-2517A7.TF CITBI-E1 Homo genomic survey sequence.
AQ275866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 301 838 0200
Fax: 301 838 0208
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Map Building
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GAACGCGCTGCTACACT-CAGTCTGGGTGACAGTGCAAGAAGCTGTCTCAAAAATMATAA
                                                                                                                                                                                                                   ATAGCTTGAGTCCAGCAGTTTGAGACCAGTCAGGGCAACACAGCAGCAGACCCCATATCTAA 3402
                                                                                ACAGGAAGCTGAGGCAGAAGGATCACTTGAGCCCAGGAGGTTGAGGCTGCAGTGATCCAT 3522
                                                                                                                                                                                                                                                                                        TAGATGAGTGTGGTGGCTCATGCCTGTAATCCCCAACACTTTGGGAAGCCGGGTCGGGAGG
                                                                                                                                                       AAAAACAAAACAAAACTTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTAC
                                                                                                                                                                                          ACAGCTTGAGCCCAGGAGTTTGAGACTAGCTTGGGCAACACAGGAAAACCTCATCTCTAC
                                                                                                                                                                                                                                                                 TGGCTGAGTGTGGTGGCTCACACCTGTAATCCCAGCACTTTGGNAGGCTCATGTGGAAGG
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                                                    TCAGCAGGCTGAGGCAGGATGACATGAGCCCAAAAGGTTAAGGCTGCAGTGAGCCGT
                                                                                                                       AAAAAAAATTTTAAGAAAGTAAACGGGAGTGGTGACGAACACCCATAGTCCCAGCTAC
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ss: BAC ends.
                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="sperm"
/clone_lib="CIBI-EL"
/nore="Vector: pBeloBAC11; Site_1:
CalTech Human BAC Library D"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            crganism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2517A7"
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(Cercopithecus aethiops
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Cercopithecidae;
(Cercopithecinae; Cercopithecus.
1 (bases 1 to 725)
Minhas, R., Zhang, X., Dore, C., Villeneuve, A., Lepage, P.,
Forgetta, V., McKee, K., Ophoff, R.A., Fairbanks, L.A., Freimer, N.B.,
Ervin, F.R., Palmour, R.M., Hudson, T.J. and Dewar, K.
UCLA, MCGQ/SS-Xittes Vervet Monkey Mapping Project
Unpublished (2003)
Other GSS8: MUGQ CH252P002Q4SP6 H05 CD315 036
Contert, Dawar K.
Co
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MUGQ_CH252P002Q4T7_H05_CD314_036 CHORI-252 Vervet Monkey Library
Cercopithecus aethiops genomic clone CH252-2B10, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      740 Dr. Penfield Room 7214, Montreal, QC, Canada, H3H 1A4
Tel: 514 398 3311 x00089
Fax: 514 398 1795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McGill University and Genome Quebec Innovation Centre
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                                                                                                                                                                                                                                                                                                                      GATCATGCCACTGCACCCCAGCCTGGGCAACAGAGCAAGACCCCTGCCTCAAAAAAGAAAAA 340
AAACCITTIAAATITITAAAAAAATAGATGAGTGTGGTGGCTCATGCCTGTAATCCCAA 3317
                                                                                                                                                         TAACAACTATTGAAATCATGACATACGTTTAAATGATATTATTTAAATACGTTAGGCTAT 3257
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te: 2 row: B column: 10
primer: T7: TAATACGACTCACTATAGGG
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/dev_Btage="Adult"
/clome lib="CHORI-252 Vervet Monkey Library"
/clome ib="CHORI-252 Vervet Monkey Library"
/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoR1;
/note="Vector: pTARBAC2.1; Site_1: EcoR1; Site_2: EcoR1;
/constructed by Michael Nefedov in Pieter de Jong's
laboratory at BACPAC Resources, Children's Hospital in
Oakland Research Institute."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Cercopithecus aethiops"
/mol_type="genomic DNA"
/db_xref="taxon:9534"
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Pred. No. 1.5e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Volik SV
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 7665
Email: svolik@cc.ucsf.cdu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WHABFGITR Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-8K2, genomic survey sequence.
BZ601705
BZ601705.1 GI:31510167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 828)

volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Kowbel, D., Huang, G., Lapuk, A., Kuo, W.-L., Magrane, G., de Jong, P., Gray, J.W. and Collins, C. End-sequence profiling: Sequence-based analysis of aberrant genomes Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (human)
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                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="MCF7_1-8K2"
/sex="female"
                                                                                                         (MCF7_1)*
(note="Vector: pECBAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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   3.0%;
   Score 180;
Pred. No. 1.
   DB 28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoni; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 733)

Adams, M.D., Rounsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K. Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C.
                                                                                                                                                                                  Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or fi
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.ht
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                       Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0208
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of BAC End Sequences for Sequence-Ready Map Building (1998)
Unpublished (1998)
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RPCII1-42023.TJ RPCI-11 Homo
genomic survey sequence.
AQ052879
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTGGTTCATACCTATAATCCCAACACTTTGGGAGACTGAGGCTGGAAGATCACTTGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGGCTCATGCCTGTAATCCCAACACTTTGGGAAGCCGGGTCGGGAGGATAGCTTGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APATTGATTATTTGGGAGTCTATATCCCTGGAAGTTAATTTAAAATATTTAGAAGAGT 3711
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                                                      /organism="Homo sapiens"
/mol type="genomic DNA"
/db xxef="GDB:7516102"
/db xxef="taxon:9606"
/clone="RPCI-11-42023"
     /cell_type="Lymphocytes"
/clone_lib="RPCI-11"
                                                                                                                                                                ocation/Qualifiers
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VERSION
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ORGANISM
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Best Local Similarity
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                                                                                                                                                    cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2398 row: 1 column: 22
High quality sequence stop: 542.
                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgspbs-r@mail.nih.gov
Tissus Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9691256
AGENCOURT 8176628 NIH MGC 110
5', mRNA sequence.
BQ691256
BQ691256.1 G1:21816572
                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 567)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buceleostomi;
Mammalia; Eutheria; Primatee; Catarrhini; Hominidae; Homo.
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                                                                                                                                         quality sequence stop: Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/mb ref="caxon.9606"
/clone="IMAGE:6252453"
/tissue_type="ductal carcinoma, cell
/lab host="BH108 (phage-resistant)"
/clone_lib="NIH_MGC_110"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pBACe3.6; Site_1: EcoRI;
RPCII1 Human Male BAC Library"
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sapiens
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linear BST 15-JUL-2002 CDNA clone IMAGE:6252453

3495

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REFERENCE
AUTHORS
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ORGANISM
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AQ780966
LOCUS
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Best Local Sim
Matches 257;
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PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A0780966 B10 bp DNA linear GSS 02-AUG-1999 HS_3138_B1_D10_T7C CIT Approved Human Genomic Sperm Library D Homo sagiens genomic clone Plate=3138 Col=19 Row=H, genomic survey sequence. A0780966 A0780966 A0780966.1 GI:5683926 GSS.
                                                                Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109,
Tel: (206) 616-388
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics
BAC end Web Server: http://www.htsc.washington.
                                                                                                                                                                                                                                                                                                                                                                                                                   Bukaryola: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 810)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a)
Plate: 3138 row:
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                         Sequence-tagged connectors: A sequence approach to mapping scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                    Hood, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAACAAAACAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACAC 3464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTTGAGTCCAGCAGTTTGAGACCAGTCAGGGCAACACAGCAAGACCCCCATATCTAAAA 3404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANATAANATAACTTTTAAAAAACAAAAATTAATTAAATTTAAAAACACAA 3635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGGAAGCTGAGGCAGAAGGATCACTTGAGCCCCAGGAGGTTGAGGCTGCAGTGATCCATGA 3524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTTGAGCCCAGGAGTTTGAGACCAGCCTGGGCAACACAGCGAAACCCTTTCTCT----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.0%;
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Pred. No. 2.5e-16;
0; Mismatches 88
                                                                                                                                                                                                                                                                                                                                                                                                              Furlong, J., Young
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                                                                                                                                                                                     98109,
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                                                                     (info@resgen.com)
.edu
                                                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                                                                                                                                   Holzman, T.,
Adams, M.D. and
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BQ688837
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5', mRNA sequence.
BQ688837 BQ688837.1 GI:21814153
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Location/Qualifiers
                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 637)

NHH-MCC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: coapsbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
DNA Sequencing the I.M.A.G.E. Consortium/LLNL at:
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCN2386 row: 1 column: 02
High quality sequence stop: 636.
                                                                                                                                                                                                                                                                                  Homo sapiens (human)
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56; Conservative
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3138 Col=19
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Pred. No. 2e-16;
0; Mismatches 109;
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cDNA clone IMAGE:6247825
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Matches 251; Conserv
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1 (Dases 1 to 440)

NCI/NINDS-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National cancer Institute / National Institute of Neurological Disorders and Stroke, Brain Tumor Genome Anatomy Project (CGAP/BTGAP), Tumor Gene Index (Disorders Pobert Etruscher Disorders)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A1362915
qy81c16.x1 NCI CGAP Brn25 Homo s
similar to contains Alu repetiti
A1362915
A1362915.1 GI:4114536
CDNA Library Preparation: M. Bento Soares, Ph.D., Bonaldo, Ph.D. arrayed by: Greg Lennon, Ph.D.
                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: David N. Louis,
                                                                                                                                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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//clone="IMAGE:6247825"
//tissue_type="ductal carcinoma, cell line"
//tissue_type="ductal carcinoma, cell line"
//tissue_type="ductal carcinoma, cell line"
//tissue_type="ductal carcinoma, cell line"
//tissue_type="ductal carcinoma, post="ductal line"
//clone_lib="NIH_MGC_110"
//force="organ: pancreas; Vector: pOfB7; Site_1: XhoI;
//force="corgan: pancreas; Vector: pofB7; Si
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6247825"
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Pred. No. 2.8e-16;
0; Mismatches 75;
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25 Homo sapiens cDNA clone IMAGE:2018410 3'
repetitive element;, mRNA sequence.
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DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Confortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
Location/Qualifiers
Ce /organism="Homo sapiens"
/mol_type="mRNA"
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Best Local Si Matches 240; Query Match 3350 3530 3470 3410 3589 AAAATA 3594 3290 127 187 244 304 67 Similarity AAACAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGGAA 3469 GTGTGGTGGCTCATACCTGTAATCCCAGCACTTTGGGAAGCCCGAGATGGGAGGATCGCTT GTGTGGTGGCTCATGCCTGTAATCCCCAACACTTTTGGGAAGCCCGGGTCGGGAGGATAGCTT GCTGAGGTGGGAGCATCACTTGAGCCCAGGAATTTGAGGCTGCATTCAGCTATGATTGCA GCTGAGGCAGAAGGATCACTTGAGGCCCAGGAGGTTGAGGCTGCAGTGATCCATGAACGCG 3529 AAATACAAAAAATTAGCAGGGCTTGGTGGTGCCTACCTGTTGTCCCAGCTACTCTGGAG Conservative 3.0%; 0; Score 178.8; DB 9; Pred. No. 3.8e-16; 0; Mismatches 62; Length 4. 89 245 3349 128

DNA linear GSS 03-NOV-2001

FINITION Pan troglodytes DNA, clone: PTB-065D24.F, genomic survey sequence.

CESSION AG073447.1 GI:16625249

SYMORDS GSS.

Pan troglodytes (chimpanzee)

ORGANISM RETURN METAZOA; Chordata; Craniata; Vertebrata; Buteleostomi; PERENCE NAMERYOTA; Metazoa; Chordata; Catarrhini; Hominidae; Pan.

1

AUTHORS PUJ1yama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

TITLE BAC end sequences of Library PTB

JOURNAL Umpublished

2 (bases 1 to 674)

EDIJYAMA,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

TOTOKI,Y., Watanabe,H. and Sakaki,Y.

BAC end sequences of Library PTB

JOURNAL Umpublished

2 (bases 1 to 674)

EDIJYAMA,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,

TOTOKI,Y., Watanabe,H. and Sakaki,Y.

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Search completed: September 27, 2004, 18:27:21 Job time: 13719 secs
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 75.9
Matches 233; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                    3529
                                                                                                                                                                                                                 3409 AAAACAAAACAAAATTACCTGGGTATGGTTGTGCTCACCTGTAGTCCAAGCTACACAGGA 3468
                                                                                                                                                                                                                                                                                                                                                                                           3349 TGAGTCCAGCAGTTTGAGACCCAGTCAGGGCAACACACAGCAAGACCCCCATATCTAAAAAAAC 3408
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                                                                                                                                         97
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Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIXEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tcl:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.

PRIMERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequencing: -21M13
                                                                                                                                                                                                                                                                                           ATAAAAAATAAAAATGAGCCAGGAGTGCTGGTGCATTCCTGTAGTCCCAGCTACTCAGGA 218
                                                                                                                                                                                                                                                                                                                                                                    TGAGTCCAGGAGTTTGAGACCAGCCTGGGCAATACAGAAAGATCCTATTTCTACCAAAA- 278
                                                                       ACTATGA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
Location/Qualifiers
1 .674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Pan troglodytes"

/mol_type="genomic_DNA"

/db_xref="taxon:9598"

/clone="PTB-065D24.F"

/sex="male"
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/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.0%; Score 178.2; DB 29; Length 674;
75.9%; Pred. No. 3.6e-16;
ative 0; Mismatches 73; Indels 1; Gaps
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